

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GLGAQIM*GQEFET
11562	25463	A	11662	142	437	GQRVQIFFFFWKRFPFFAQQGTEGAQFR LIKPSPSGLKEIPPPNPPRKGE*RDGPP FRGDFVFLRKNGVPPCGQGGSKPPAPGE PPFFTTPPRGENNRG
11563	25464	A	11663	120	353	QALQVMLKHVNNFFFLFLFWKQSFVPL PRLECNGATSVHCNLCPLG*RNFPASAQ EFRIAGSYDHAICPPASGKGE
11564	25465	A	11664	1	404	NTWSDLIISYFHPRPSAFFLRQGLALSP RLEYRGTTIGHYSLDLWGSSDSPASISR VAGTTYRCM*FQLLGRLRRENHLSRGR GCSDP*LCPYTPAWVTERDPVSKKKLRG GGENSLSSQTMV
11565	25466	A	11665	493	3	NIWIPDVLPGHARQ*LGSPGKLSAGF* PLQFPQTLSSARAPPFCRLRLQVRNTVG FLPSPHTSRPSHCLPACPLPSRTQPWVP VKPGPTACRGFLQHPPTGSPSP*SFQG SSWWDTDLRALECLLRILGRNCSVFVT TQGQLSHEGMNKEFLLTCAKKKK
11566	25467	A	11666	3	401	CMERAVTVLLPGSATQSPVYAPRALAR LWLTAAMMISGFIADYEA*SSRCSSACP AGDSLSEYHSPADSFSIMGSPVGAQDFC ADLGVSRANFIPTDDMTSTPDLQWLQV PALVYSVGPSETIAPHPLGVP
11567	25468	A	11667	1	446	LSCAKPPQRPLRHGIKIFNVFEETRAN KHLGLVSKLKPRGFPAFLSVSSFGQKK HVPQWLQSHSHILVISLDDFFFFFEK KPPFFPPGGRERDQTPFN*TPPRGG*RE SPFFPSRGGGTQGWAPHCP IIFRFQKK GVFPLRAR
11568	25469	A	11668	18	403	DPLQRPQYRGCLRSVGCQLQSPTPRGPS GRWPNPAQARGPGEAQAWAWPGGGPREA FSGQGRPPPLGLPHRRKGAGPPGPMGP *HEGQGS*GASCRGGLACTAFPAASSP PIFGGLTPPNLNFPEE
11569	25470	A	11669	157	1	PRPQGFVVFVFFFEFEMQGRLECSGAISA H*NLHFLGSSNSPASASHVYAPLY
11570	25471	A	11670	396	7	EKVCQARDKSACEGHSCADARSCLHLRV DQGGQHGSHGACPGRRLRGPDTHRQSCY QCRCNRPDLRQPGRAGTP*CAEAAAEP DAAVHPGQPAPARLPPALPGRGLPLPH PGGSQRVYCVRCIGSKLR
11571	25472	A	11671	209	3	DDLGTHRPGKSQVRVTPREAGENPSAVL PCYLHLVPFV*EDEVKPEDSIDMPGNE YAREFLAHAPLY
11572	25473	A	11672	270	101	LSLNRWILGAYIIFFETESHVAQAGVR *HNLGLLQSLPPGSRRLPAFKVAFLEFIG
11573	25474	A	11673	421	592	SSCTPGVIKIPCVRSNHMKLPGPMVA HTCNPSTLGGQGGRI TWSE*FKTRLGNM A
11574	25475	A	11674	176	6	LTFVYMPCFCALSSIMTYGLAM*FHFH SMTLFIIGVLSVALAIYQ*WLDVSRVSV
11575	25476	A	11675	1	418	NTVCVCVCVCVCVCVERKAGHRLTDSFP IQAGPGAQARTLCLRESTGGALSSGLPA SRYQDPGRGALPHCVWTPRGWNWRLNY PPARSPSREAVCYFRQTLKKWRSRPGQG GRILRVIRTASTFRDTS*TESACLGARP CLDGK*VCESVPCFSLHTHTHTHTHT

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						HCI
11576	25477	A	11676	305	698	SFMGRSPRKIDQFCNSRNMVHGSVTFRD VAIDFSQEEWECLQPDQRTLYRDVMLEN YSHLISLGSSISKPDVITLLEQKEPWW VVSKESTRWYPGK*E*SRQGEAIIIVPDS PCAQRGVTPLCGLENFLQ
11577	25478	A	11677	107	397	GGDGRETLLRAPADDGCI*QERAETPLAI SCPRSSSTCRGRARRYDGCRTDGHQLI QRGQQQESSRRTAQPGSSKLCRGGGHR PSLGTGVHGCSSL
11578	25479	A	11678	514	554	RAKPTPP*GGGEGQNFGLLKPPVSGLP LACPTPPKRWKPKPPPPAPPHLFF**K RGLIF*PGEVFNLRNWKLPSPPPQRGGN KGRNQPPPRGTFMF
11579	25480	A	11679	266	3	GPPLFLGLKN*TFFSPTKV*IFFSQVFS SFPQGLKGVREIFFFFFFFF*DRLECNGT ISAHCNLRLPSSSDSQASAGTTGVCHYT RMY
11580	25481	A	11680	1	408	NTCALRHRDHFSFWSDGKTEGEERIVQ ENWLISWNNFSPETLLTLSCPLGKEGM PGEDGTAGAGKVPGEDKIPG*DGAGED GTEDENGTTGEDETAGVGKTPGAGGTTG EDDTESEDGTTGEDETAGKGGTAG
11581	25482	A	11681	244	420	KDSESTKAYIRDNISSTKKKSWPGAGA HPCNPSTLEGKGG*IT*SQEFETSLANM VKL
11582	25483	A	11682	294	443	QMNTCTHIQPAYVH*EKYFRPSAMAHAL NPSTLGGRGWIT*SQEFQTRP
11583	25484	A	11683	346	1	YNTNQFTLRGTQASVYTCLTALIVLKL NQPYTLASVLLNAGNQPFHAFSPPSLH PDAFHSKIMSHIIILLGFIPFLPASQS LTLSPSLERSGTISAQCNLCPLGSSNSP ISA
11584	25485	A	11684	140	423	SSHQASSPPTTASHSMKISVAAIPFLL ITITLGTKTESSSRGPYPHSECCFTYTT YKIPAQRIIMDIYETNSQCFKPGIVFITK RGHSRWTNPK
11585	25486	A	11685	163	3	TKIPCNRLKFGPPSCCGFFFLPFPFF FEETLSRSVAQAGLOWRDLGSLAL
11586	25487	A	11686	179	1	PIVFLGMLFVAFARFPFESVTKPPNFF FFFEMESCSVAQAGVQWRDLGSLQARPP RST
11587	25488	A	11687	192	1	EQGFDPGLASWISLKD TAKWNGDELCS YYQSCCTDYTAECKPQVTRGDVFTMPED EYTVYDDG
11588	25489	A	11688	89	3	SGGYCCCLCCCRSRYSCCCRLREGPTK
11589	25490	A	11689	168	2	QDRLQPHESKRKLGAPAPQLRSEDTPS VVNFQSTESQLMSKGBDETKDDSKETV
11590	25491	A	11690	301	397	HFVFSLV TGMNPLSPYLNVDPRYLQVR LRFY
11591	25492	A	11691	18	421	TKALQITCYLHSTMSEESDGKLIEDSLI QLRCHFTWKLLIEAPEIPDLNRIWEEI QFLDTKYNVGIHNLAYVKHLKGQNEEA LVSLKKAEDLIQKEHANQADIRSLWTG NFAWVYYHMGRLAEAQTYLDKV
11592	25493	A	11692	188	3	PLQGGKFGAKERGQKKGFLRGGVASRP RPPFGPSLFFFFFFETDSHSAQDGVQW CDLGS

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11593	25494	A	11693	24	391	APRADAMGHFTEEDMATITSLWGQGNVE DAGGETLGRLLDVYPWTQRFDSFGNLS SASAIMGNPKVKKAHGKKGLTSLGDAIQH LDDLKGTFSQLSELHCDKLHVDPENFKP LGNGLQTALQ
11594	25495	A	11694	138	425	NSGVKAAFQLNPGNPNEGKPGPGFKTH PGQLGETHFLKIHYSGLVGKPWESQL LGNLNRNHWTPERGGPRDLRHCHGIQP WATNGNFVLKKK
11595	25496	A	11695	158	838	CGTVHSCDAGQRQATAPSHPCDHGNQQ PILYRVLCCQLFWILCFVFSHSIMSTKC PSVSPVSGEMKKRKAITLEMLKIIAQH EGGKPVMAIARELGLWQSTISTILRDKK QISDAAKSSASVKSTVITKKRAGPIDDM EKLVMWMEDQIQKRIPLSLMIQAKAR SLFNMLKDRASDPTYTQMFKASHGWFQR FKRRHNFHNVKITGEAARAGNEGAIAFK EQL
11596	25497	A	11696	834	1431	SSACQGSQGWPPRQFWMWGSRRAPS VTHRTGERCSTSGSAPLPLLLSSLCSSL PRSWEHSTLRQPPHPPLPPGCLPPGRE AQRLSGAGHGPGRPAASYPDTQADR KQQQHHPGPDQHVGHREGLAEDAATHL GLVAALSCWLLGRAEAGYQVPHGHDHPK DQHPQADGGQRIVRAIGLGLGHHVSGRR ARP
11597	25498	A	11697	143	1	ISKERGASRFSGPWVFFFFFFLESRSVAQ AGVQWCNLGSLQAPPPGFT
11598	25499	A	11698	58	459	KGKEEKVKRKEAEQNFSPYAQDKQERIK GNENDEKTKQGKETIIDIELFKGLDETG ENMDSTLRTPTPEPLENNKQILVLGLDG AGKTSVLHSLASNRVQHSVAPTLGFHAV CINTEYSHMEFLEIGGSKPFRS
11599	25500	A	11699	215	1	GTKKALWAGGGGFFPYLPPMGPLGPICG GVGKGSPLGCPPIFFFFFFETESCSVA RLDAQWPDLSLQSP
11600	25501	A	11700	300	420	KPKILFGNVFAAPHMENLKRGETVAKE ISEAMKVKAMC
11601	25502	A	11701	351	466	RIKNADLSQAQWFTPVIPALWEAKVGRS LEVRSSRPVW
11602	25503	A	11702	172	400	SNRLRNKIQGVFLNDSSISPFILRKQSI GQAWWLTPVIPALWKAASGSPMDSTT LLPSSSQVPSLVKMEKLNYS
11603	25504	A	11703	284	408	ASVFSSFFVCLFVFEMESRSFAQAGVL WRDLGSLQAPPPG
11604	25505	A	11704	20	447	LPGADYGGGHLRLFLHLLASAAWVPD ESQVTLSAICVLSTVLIMEFPDLGKHC SEKTCQQLDFLPVKCDACKQDFCKDHF YAAHKCPFAFQKDVHVPVCLCNTPIPV KKGQIPDVVVGDHIDRDCDSHPGKKKEK IFA
11605	25506	A	11705	1	455	HS CSLQFTPTAWDCTGSVSSEQGERPAA AMKICSLTLLSFLLLAAQVLLVEGKKKV KNGLHSKVRSEQKDTLGNTQIKQKSRPG NKGKFVTKDQANCRWAATEQEEGISLKD ECTQLDHEFSCVFAGNPTSCPKAQDERV YWKQVARKLRS
11606	25507	A	11706	1	428	DAEADKMAAAVRGGRSGSGGCSGAGG

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						ASNCGTGSGRSGLLDKWKIDDKPKVKIDK WDGSAVKNSLDDSAKKVLLKYYKVENF GLIDGRLTICTISCFFAIVALIWDYMHP FPESKPVLAALCVISYFVMGILTYTSY RE
11607	25508	A	11707	1	422	RSQARSSAAAAARASVPLRGSPGPSAIM PMFIVNTNVPRASVPDGLSELTOQLAQ ATGKPPQYIAEHVVPDQLMAFGGSSEPS ALCSLHSGKIGGAQNRYSKLLSGLLA ERLRISPDVYINYYDMNAANVGWNNST
11608	25509	A	11709	88	423	AADAMKQAEEMAGAFMRLAYQELQIDRL KEDKMLLNLEGNKREHAERLGMGLVSR SVSHSVLSEMLVIEHETPVSAKSSRSQ DLFDDVGTFCSGPSKYTDNPFSLWESIG
11609	25510	A	11710	393	130	NPSATAQSFHLAARKLSTLDRPGSQAPQ KPMPSPKPGVVLPASTNAVPTPLAEATP SKAHPAISLLSTEELGIFKAVPSPASSCS FLHV
11610	25511	A	11711	331	440	KIFFLNFLISRWWCAPLVLATWEAEVG ESLYPRRS
11611	25512	A	11712	122	478	SGLCPQQPPRANSCPPSSMASCAEPSEP SAPLPAGVPPLEDFFELVDGVEDAQGE EDEEEEEEDDLSELPLEDMGQPPAE EQPGALAREFLAAMEPEPGPSVPKEWL DILGNGL
11612	25513	A	11713	102	2	TNLGNPRRPPPPFFFTETVSLLAQAGVQW CDLGS
11613	25514	A	11714	126	2	FFAPFLKIFFFFFFFSEMESC SVLQAGVQ WHDLGS LQNEGSQ
11614	25515	A	11715	178	449	LSGGNLFGTIILLYCAIIGKLLGLIKL PTLPPLPSLLGMLLAGILITNIPVINDN VQIMHRWSYSLRSIALAILVRAGLVLE SKALEK
11615	25516	A	11716	48	417	GSGGNHNSVCCDTMEGGGGSGDKTTGVLA GFFGAGEAGYSHADLAGVPLTGMNPLSP YLNVDPRYLVDQDTEFLPTGANKTWGR FELAFFTIGGCCMTGAAFGAMNGLRLGL KETQNMASKP
11616	25517	A	11717	103	2	PKSPTQWLMAVIPALWEAKAGGSRESRS SRPAL
11617	25518	A	11718	1	413	WPSGQVLVGCLSFSLYCWKRS LKRNPG FEVLLKIFLKNHPRCHTNRMQLTATPV SALADEPAHIRATGLIPFQMVSFQASLE DENGDMFYSAHYRANFAEADLNHAAS LGGDYLGDLALRLCTLEPVFPQSY
11618	25519	A	11720	116	462	AGMLPAVGSVDEEEDPAEEDCPVLVPIE TTQSEEEKSGLGAKIPVTIITGYLGAG KTTLNLYILTEQHSKRVAVILNESGEGS ALEKSLAVSQGGELYEEWLELRNGCLCC SVK
11619	25520	A	11721	167	407	EIYSLTRFIEVKMSKKISGGTVVEMLGD EMTRI IRET LKEKLIFPYVESHLHSYDL GIENRDATNDQATKDALEAFNKP
11620	25521	A	11722	254	423	NQLSSIMAMFKKIKSFVVFNDEPKVYG SGEKVAGRVIVEVCEVTRVKAVRILACG
11621	25522	A	11723	3	424	VSCDTMEGGGGSGDKTTGGLAGFFGAGG AGYSHADLAGVPLTGMNPLCPYLNVDPR YLEQDTDEFILPTGANKTRGKFELALFT

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						IGRCCMTGAAGFAMNGLRVGLKETQNM WSKPRNVPIIDMVTROGALWANTLGALA
11622	25523	A	11724	2	343	AFGTMKWWTLVSVLFLFSSAYSRGVFR DAHKSEVAHRFKDLGEENFKALVMI QDLQQCPFEDDAFSTSEVPEFATTCQDD DHFEDRCRRVHTLVVVQLCTPATLLET DY
11623	25524	A	11725	1	359	HAFGTMKWWTVISLVFLFNSAYSRGVFR RDAHKSEVAHRFKDLGEENFKALVLI AHYLHQCPFEDHVKLVNDVTEFAKT DESAENCCKSLHTLFGDKLCTVATLQ ET YGEMADC
11624	25525	A	11726	1	349	GAMSDRKFSAPRHGSLGLFPRKRSIR HR GKAKSFPKDDPSKPGHLTGFLGY KAGMT HIVREVYRPGSKANTNEVAE AVTIVETP PMEVDIAGYMETPRGLR TFNTAFAEHMSDEC
11625	25526	A	11727	81	349	TKGSVVSCCVCLCVCLCTWSHLCL RLVTWLPDMPDDVLWLQWVTSQV FTRVLMCLLPASRSQMPVSSQAS PCTPEQDWPCWTPCSPEGC
11626	25527	A	11728	264	388	QADPKDIMKFPGLNQLRSLFLEKAIT REAQMWKVNVKRM
11627	25528	A	11729	2	471	PGCSASWSKRGSGPMDLSSMAAAG SVKALQVAEVLAEIVSCCVGPEGRQ VLCTKPTGEVLLSRNGRLLLEALH LEHPIARMIVDCVSSHLKKTGDGAK TFIIFLCHLLRGLHAITDREKDP LMCENIQTHGRHWKNC SRWKFI SQALLTFQTQIL
11628	25529	A	11730	160	377	LQGFGRPSVYHAAIVIFLEFFAWGL LTT PMLTVSIAELGLCFVRERD KFLGTYHCVCLDTCGLVALDSDLKQ
11629	25530	A	11731	45	438	KLQGRKEATVTKESCKSKSRKVGSP DRFRSPQKRSGRQDCFTLFCFWK VLDKNMELISPTVIIILGCLALFL LLQRKNLRRPPCIKGWIPWIGVGF FGKAPLEFIEKARIKVCGRGRRGL QRRQCFLF
11630	25531	A	11732	169	292	DSILLVNLACSAVISAHCNLR LPGSSDSPASASRAAGGAHL
11631	25532	A	11733	473	600	KFWEKRTEGRGKSKSKNSETGEI VSISALSTTEVAMHTSTSS
11632	25533	A	11734	19	349	APSPDAMGHFTEEDKATITSLWGT VNVEDAGGETLGRLLGDYPWTQ RFFDSFGNLT SASAIMGNPKVKA HGTVLTSLGDAIKHLDDLKGTFA QLSELHCDKLLVDPENF
11633	25534	A	11735	234	359	FYHLKSFTVSSVQSRWLTPVIPAL WEAEAGGSPPEVKSSRPAS
11634	25535	A	11736	15	372	KLPLKALTGEEKTHINIDIIGHVH SVKSTTGHLIYKSRGIDERTIEIFE KEAAEMGKGSFKYACILDKLAER RERGITIDISMRKFETSKYYVTI IDAPGHRDFIKDMTTGTSHADCA
11635	25536	A	11737	1	357	IWKAAAMASPAGSWARPPRPMREP QTLAMPTNAAEDQKLKLERLMKSP DLAVTIPEKMSEWSPGPPPEFDRD VMGSRAGAASGEFHVYRLLRREY QRQDYMDAMAEKRILDAEFQRRLE
11636	25537	A	11738	24	335	APNANAMGHYTEEDKATITSPWGK GNVE

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						DAGGKTLGRLLDVYPWTHRFFDFRGNLS SDSAIMGNPDKAHGQKVLTS LGDATKH LDDLKGTFAQLSELHCDKLH
11637	25538	A	11739	141	335	MQFLPCIPILKSLEKSVASHSQTVHSDI ISTVEFNHTGELLSTGDKGGRVVIQRE QESKNQVHR
11638	25539	A	11740	7	337	APSPDAMGHFAEDKATITSLWCKVNVE DAGGETLGRLLAVYPWTQRFDSFGNLT SDSAIMGNRKVNAGTKVLTS LGDAIKH LDDLKGTFAQLTELHCDKLHVDPENF
11639	25540	A	11741	182	360	SRHSISPPVNQIQLGASVTEELTVVTKT ARVSRAQWLMPIPALWEAEAGESPEVR NSR
11640	25541	A	11742	174	1	HFSDSLFLVCVRQDLTLLPRLECSLIT AHC SLHLGSGDPPTAASWVSGNTGVHY HA
11641	25542	A	11743	75	218	KTILGRAQWMTVIPALWEAKVGRSPVS ASQSAWDYRREPPCPSCTI
11642	25543	A	11744	168	2	LAPLWSLGPVLGGVGQSGPGPFFFFFFF FFFFFFESC SVARLECSGPILAHCSLR
11643	25544	A	11745	83	2	REQRFLLPFVQLCPAPRGGVYRGRQAS
11644	25545	A	11746	156	3	FHSGSGRVENPSFFFSFFETGSCSVTQD GECTGATLAHCDLCLFGSSNSS
11645	25546	A	11747	244	330	KDRAQWVTPVIPALWAAKAGRSLEVRSS R
11646	25547	A	11748	201	1	TSQPLIRITLSTFFFFSRDGGTLMLPRL DPELPGSSNPPSCSASRVDTTGMCHHT RLIFFSQTDKK
11647	25548	A	11749	262	3	VYTSLTPPPISVNLTLQVSPRSVSYEQN ILCLLFVITYFTCTFFVCLFVCLFVCFK MESCSVAQAGVRWRDLGLLQAPPGFTY TT
11648	25549	A	11750	225	3	PIINFSVPQFLHLYNGIIESTPPSCCI LKCQSLGQAQWFTPVITTLWEAEAGRSL EAWTLKTILANMAKPHL
11649	25550	A	11751	185	2	VSTPFNSFPSPWDLVFLKGFFFFFFFFF FFETEFCSPLERNGAPLAHCNLR LPR SSNSP
11650	25551	A	11752	261	336	DRVSLWSPRLECNGAISSHCNLR LRP
11651	25552	A	11753	282	381	TDLLYKKKCGLGAVAHAYNPSALGGQGG RITCS
11652	25553	A	11754	202	45	NERKVKLQWALILPLPFLNGQLKSRFQ KKKKKKKKKKKEKRRKKTLVVIC
11653	25554	A	11755	293	357	LTPVIPALWEAEVGGSPVRS
11654	25555	A	11756	264	1	TLPIINVCCDHSTGPSLSLSPLLSLPYS LRHNNIEIRLINNPTTACKYSCLKKSHK SLTLDQKLEMIKLGEGLLKAQIGQLG LLHQ
11655	25556	A	11757	126	1	ILPGFLKELKIELPFNPAILPLGIYPKE KKLLYQKDTCTHMF
11656	25557	A	11758	399	226	IEKGTGRVWLTTPMIPALSEAKAGGSPE VRSPRPACIGLLKFWYYRCEPQHPARLS EI
11657	25558	A	11759	235	380	DTTVLKLGLITLQWASKCSSERKSRTS LTLTQKLEMVKLSEEGMSKGD
11658	25559	A	11760	249	357	NRASGQTWCPTPIMPALWEVEAGGSLEP RSLRLTWA

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11659	25560	A	11761	168	372	KLHCLLCFYLSSEFFVFCFLETSLSLVAQSKCSGTVITHCSLKLCCSSDPATSDSRVAETTGTGYHAGL
11660	25561	A	11762	303	377	QFAGCRWLMPVIPALWEAKADGSPE
11661	25562	A	11763	135	1	ATTPGLFFIFYFFETESHSAQAGVQCMISVHCNLCCLPGSSDSPV
11662	25563	A	11764	219	2	KLRSSQLSEPEVRPDSTLSMLMHARAHTHTHTPHLFLPHPCSRPHTSTPTCMPIVTHSPIYLKFKHSHTYIL
11663	25564	A	11765	102	1	NRPINNPTMASMCSSERKSHKSLTLNQKLEMIKL
11664	25565	A	11766	245	3	PGEPEEDQLVKFRPSLLWVFMFLFLRRSLALSPRLCESGVECSGVISAHCNLCITGFKQFSCSLSLSGWDYRHPVPCPS
11665	25566	A	11767	350	97	GSVPASPQVTRPTLMTSLADKWFSLCLTSLRVNFGVALILSGSHSVSQDTLDDLTLFSTHLGLPKCWDYKRVPCSAQFLVTFLLGSVAGDLLCFFGGVIFPCSFMFMSLICYLYIWNVCVFLFFKTEPHFVTHSGVHWCDDLQPPPPN
11667	25568	A	11769	131	2	YTLYIPNKSPIENIQLSWAQWLVPVIPA LCGAETGELEPRSS
11668	25569	A	11770	165	1	VLIPLIHLCIYIYIYIYICVYIYTRIYT HICITHVYIHIYVYIHTYIYTYMYTY
11669	25570	A	11771	72	1	ILLFFFFFFEAESCSVAQAGMQWCN
11670	25571	A	11772	121	3	TSEVLFCFETEFCSCCCGLCNGAILAHCNLRPLPGSSD
11671	25572	A	11773	152	3	HVCLNLTLPPLFEKNIFSLCVCVCVCVCVCVVLCKKKCKEKFYFERTF
11672	25573	A	11774	190	2	GFSPRQRGAPRVPPPLAGFPPIFFFFFFFEMWHSVAPAGVQWCNHSALALTSPLDSGDDP
11673	25574	A	11775	287	1	GAHRRKLFITPGESLRDKQIAGFEHRRGGEKKKTLFYKKKKKKKKRKEKKGKMKMLPKCNYTMKNHQVPYSIRPTRECADLRV FYFIKFQILKY
11674	25575	A	11776	121	3	KCASRDLSKFFFFFFFLETESRSVAQAGVQWCDLGSLLQAL
11675	25576	A	11777	142	1	EKTLHVRNTIHNSEGLVIKIHGRLGVV AHACNPSTLGGRGGQITRS
11676	25577	A	11778	179	3	SHQPVPGTLDLPRGPQKLQSTSEAESEA SMSEASSEDLVPPLEAGAAPYREEEEA AKK
11677	25578	A	11779	147	6	KTPGLKKNSNFFFFFFFETRSHSTARA GVRGCDLSSIQPPPLGLK
11678	25579	A	11780	184	3	GFGFYIIPNYRLFFFSLLIGPFFFLIFF ETEPCSVARLECSGVISAHCNIRLLGSC DSPA
11679	25580	A	11781	120	319	VKSLAKFLVNYQLHRQTCSGQAGRGALR QRFGPRQVDHLRPGVRDQPGQHGETPS LLEVRKLSSG
11680	25581	A	11782	91	3	YICLSLIYTHTHTHTHTHTHTHIYIVC V
11681	25582	A	11783	221	332	SRLGMVDHPRSGVRDHPGQHGETPSLLK IQKLARRSG
11682	25583	A	11784	243	379	LKYSVPICKCKPWPPTWDHTRNPSTLGG QGGWITLDQKFETSLAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11683	25584	A	11785	327	5	GRVDSQPIYPKNPPGSFPKIYPGSFKTL FPYLOSRHSFSIPRSKLARFHQAKPLFC SKPSQSLSPHSELKKKDLQARWLTPVI RALWESKAGRSPEVRSRPTWPT
11684	25585	A	11786	245	359	FKGMDRLRSGVRDQPGQHSKTPSVLKIQ KLAGHGMRL
11685	25586	A	11787	356	67	RDIASITARLRYDRGVGTRLEVLKSD EYTKGSVLDFSRETEPIGYIYIYIYIYI YIYIYLHSLPLNHMETSLGHPPLSNNKF VQNFDSPKLSYH
11686	25587	A	11788	103	3	KYIIPVCIFFFETESCSVTQSGVQWCE LRRRG
11687	25588	A	11789	136	1	VHQFTIRILNYYYYYFFETESYSVTQAG VRWCNLGSLQPLPPGFK
11688	25589	A	11790	291	163	SLLLPLRLECNSTISAHNPRLLGSSDS PASGRSLEPRSSKLQ
11689	25590	A	11791	107	2	IFMYVFFETESRSVAQAGVQWRYLGSVQ APPSGFS
11690	25591	A	11792	329	3	KNPRNIIGKSRGPYITNFPDGKPKNSS PRGNDLSINKNWAQAFQPRGQKLFPPK KKKKKETQSR SIPRLECNPTIAQCNLK LLASSNPPTSASHSAATISMSHSG
11691	25592	A	11793	213	3	ISPWLFLLLQATLFRSQYGPFPFSL PYLFPFKQKLGSGFFFLFFFKTESRF LARLECSGIITAQ
11692	25593	A	11794	1	400	KRAAPQPAPEQRDLKKKKKKPPLAPSSL FRFWEKLLPSFQFRQPRGPFGLTRGVSF AFHRRRFWQYGNMGEKQTWGNPGSSNP PPGTAGSLSGNRGPWGCKIADRFWLYA RDSFGHSRGLKGCQAHGK
11693	25594	A	11795	3	769	RKEQTRNARAEVLRQAKANFEKEERKE LKRLRGEDTWMLPDVNERIEQFSQEHVS KKKKKKDKHKKAKKEKKKKSKKQKYEK NNESSDSSSSSEDEWVEAVPSQTPDKEK AWKVKDEKSGKDDTQIKRDEWMTVDPM SVKTVSSSSSLKAEKETMRKIEQEKQAL EQSMEIFQSKLEDAEKAASKEDYRRER WRKPTYSDKAQNCQESRESDLVKYGFCS RDRYATTD TAKNSNNEKFIGDEKDRPG SLE
11694	25595	A	11796	110	13	HTHTHTHTHKHTHTHTHTHKDRSGKIKC VPTV
11695	25596	A	11797	184	2	SEIFGKFHVFIYILT VHFMPPTQVYVERD VLGQEQLLTPVIPALWEAKAGRSPEVRS SRPA
11696	25597	A	11798	83	387	GERRRRRRRLWAPLQKKKKKKKKKKKK KKKKKKKKKKGGAPLKKPPGGPHFSGG RQKNIPPLKGELKRAPAGDFKNPGRGK IARGGFFEKNLSWGGEK
11697	25598	A	11799	153	2	IPWEDTVYSGYPQFLFSHFFFYFFFE TGSCSLTQTGVQWCNHSGLQPR
11698	25599	A	11800	93	3	VWGRAWWLTSVISALWEAKVGESPEVRS S
11699	25600	A	11801	115	1	NPLFFFFFFFEMESCSVAQAGVQWCNLG SLQPLPERFK
11700	25601	A	11802	295	137	RCFIFILFINKLYFVYLFYFFEMESHT VAQAGVQWRDLGSLQAPPPNKLYF
11701	25602	A	11803	287	1	MGPAPFKGTCCGGFQDFRFXNLEISAGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						THSPLLAQNFRVGA VPSPRYS PRFGSKG GGGFFFFFFFFFETESHVAQQAGVQWCD LGSLQALPPGF
11702	25603	A	11804	202	3	WSVCCFKQGLGLSPRLECN GAPGFKQSF PLSLLSNWGYRGPPRLNFFFFFFFFEMES CSLAQAGVQR
11703	25604	A	11805	3	315	FMLLILTLFLLRNDRLVQCDVRSSVVC GFLLGWSVILYPLMAAFMPTMWIFLFI FSMLFFYVFFLFLFLFLFLYSFPLFCF FFCFYLFREFFFFLFIFFSSP
11704	25605	A	11806	126	3	KRGFFFFFFFFFETESRSFAQAGVQWC DLGSLQALPPGV
11705	25606	A	11807	130	2	QSIKMTCSLYFFIKKNVAWWLTPVPA LWEAGAGGSHEPKS
11706	25607	A	11808	149	1	GGKKAILFFFFSLSPRLECSGAIPTHCK LCLPGSRHSPASAFRVGTAG
11707	25608	A	11809	258	3	KYYYQGNRQIKFVNAKSNKNLPSYSQKA SWFSSRNIRMMGQHQPMLDNPSTFIKK LGQAWLRLPVTIPALWEAAGGSLEBSRL
11708	25609	A	11810	153	285	CASPIRSHQKLNKNGVQWLMPTVPVW EAETGGSLQLRSSRLA
11709	25610	A	11811	160	3	NHLFLLLNRYKSI FIGRVQWLMPVSSAF WEAKAGRSFEPRSSRPAGQHGTKL
11710	25611	A	11812	89	2	AAAAAAAAETVSCSVAQGGVQLCHLHSLQL N
11711	25612	A	11813	254	336	LLGQPQWLTPVIPALWEAAGRPSEVR
11712	25613	A	11814	108	2	CVGVLGFFVCLFFETESCSVAQAGMQWH DLGSLH
11713	25614	A	11815	166	289	SHSGWNAVWRDGS LQPLTPGFKRFPCLR VPSSWDHKCAPPC
11714	25615	A	11816	192	2	DKDPGKVTRPFLLLCIFLYFICLFLRRT LAVSPRLEFSGRGCSEPRSHRCTPSWVT EQDSCRK
11715	25616	A	11817	228	343	LLQYSIQNEDAGWAWLTPVIPTLWEAK AGRSLEVRSL
11716	25617	A	11818	322	407	VLRMLLHCLRECKLVQPLWKTVMQFLKD
11717	25618	A	11819	119	1	WEKIVRGKKCKQKENTHTHTHTHTHTHT THTYRESKRERLV
11718	25619	A	11820	269	1	FVQVFYILWTQSFCLTCCQWFLLGHYLS SVSNRFRMRSGKSTFFMTSEFFFFEMES RCVTQARVLECSGISAHCKLHLPGRPH SPALV
11719	25620	A	11821	217	389	EHITVYGKLGISEHWGKGGLFNKWLTI WKKDYSWQWMLMPVIPALWEAEVGGSRV H
11720	25621	A	11822	188	1	GSHMPCRVISSVHESMNEFFAVPTSYPA NPQPRERAWRNQREKEDKKERSQRSVGR VQAGLV
11721	25622	A	11824	126	3	KLQGGVQWLTPVIPAPWEAAGRSPEVR SSRPASTWRNLV
11722	25623	A	11825	224	3	ALITIKKEVSAMELEGSNRIQAYGVQSIT GARDYHAAASRVPAIKGTHHHARVIFVF LVETGFHHVGQAGLDSC
11723	25624	A	11826	3	364	HELPEPLRVLTARVAMAPGSRSLLL AFALLCLPWLQEAGAVQTDPLSRFLDHA MLQAHRAHQLAIDTYHEFEETYIPKDQK YSFLHDSQTYFCFSDSIPTPCNMEETHQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KSNLELLR
11724	25625	A	11827	2	376	ARELPEPITVLRTAHLKAMAPGSRTYLL LAFALLCLPWLQEAGAAQTDLYMLFDH AMLQAHRAHQLAIDTYHEYDETYIPKDH KYSILHDYQTSFCFSNSITTPYNKEETQ QKSNLELLRISLL
11725	25626	A	11828	288	3	IHTKNPSVHHHHQRPKVDKTTKMGKKQS RKTGNSKKWSASPPPKHSSSPATEQSW TENDFDELREEGFRRSNYSLEQEEIQT GKEVENFEKN
11726	25627	A	11829	107	1	KRSGVRLQRLVRWLTPIPTLWEAEV GSFEVRC
11727	25628	A	11830	220	354	QGNKSFKNIIAPWLGTVAHACNPSTLGG QGGRITGHEIETILANM
11728	25629	A	11831	273	352	ENLKTGQIQWLTPVIPALWEAKAGRS
11729	25630	A	11832	239	488	SQTHCSGKTENSHGTNSDRNQVPTALHK RPSSPARFLTEAVPVPDYQLQSVAAFA VSAVASQWERTGKPFNPILLGETYELIR
11730	25631	A	11833	189	294	DQTRWLTPIPALWGAKASGSPEVRSSL HFPLLF
11731	25632	A	11834	1	332	GTSPEPLTVLWTDLLAMAPGSRTSLLL AFALLCLPWLQEAGAVQTDPLSRLFDHA MLQDHRAHHLAIDTYHEFEETIIPKDK YSFLHDSQTFFCFSDSIPTPSNMEET
11732	25633	A	11835	330	175	PRELAQLGSPNVRVSRVKPRGPQMFFF FFWRQESCSVAQAGVQWHEPEQQE
11733	25634	A	11836	96	1	VFVETGSRSAQDGGQWCDLSSLQPQPP RPRA
11734	25635	A	11837	267	334	SWVQWLTPVILALWEAEAGGSP
11735	25636	A	11838	180	2	SVLEKKEKNLYKNLFTYKLLKKVQGTQ CEGRAQICSVVCVCVSVCTCVHVCAYV SSC
11736	25637	A	11839	183	2	AAPLTSSAPQAPGWKPHLAPNSPFGNFT GRGQAQWLMFVIPALWEAKVGRSPEVRS LSSC
11737	25638	A	11840	54	330	DPNGQLPEPLKGLWTAHLVAMAPGSRTS LLAFGLLCLPWLQEAGAVQTVPLSRLF DHAMLQAHRAHQLAIDTYHEFEETIIPQ DQKNSFLD
11738	25639	A	11841	117	344	IQYVKQINETEMRNNESYLNHTSLTITI HTLCLMGSYLEHFQNCQKGRARRLMPVI PALWEAKAGRSPDVRSSKPA
11739	25640	A	11842	750	968	RAQGPRWILKIPFSSPFRFLPLIPLVFL YNSPPLFPFPRTNATNNSPFPPLPPLP LPFSPPPPSPSRPPPS
11740	25641	A	11843	757	1000	VVELVWYCCLESPFFPLPSPPLFPFPFP SPFHSFPPSPFRPPLAPTRPPPPFS LFQAPPLLPSCSPPPPPPSLSFL
11741	25642	A	11844	278	361	TLLFFFFFFEMESHFVARAEVQWRDLGS
11742	25643	A	11845	260	2	GSCLEGLTNRKDIHTKNPSVHHHHQRP KVDKTTKMGKKQSRKTGNSKKQSTSP PKERSSSPATEQSWMENFDELREEGFT RA
11743	25644	A	11846	194	2	TKFAKEPSPPPCWQEVFKTSPLGFFFCP RSFPVNGFRLKNLFFFETESCSVAQA GVQWCARA
11744	25645	A	11847	219	1	SLGHTLKQSESSLFSFPGGTPLELFKPS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VYDPSVPPFQVSKGGCVGFFFFFQTESC SVAQAGVQWHDLGSPRA
11745	25646	A	11848	126	3	RFFFKGLFLHFFFFFFFFCFETESHVA QAGVQWCDLGLV
11746	25647	A	11849	216	339	KCFKVGKVYKLNRETFYLAQNFFDRNWA TQKMVVKTLLLELT
11747	25648	A	11850	190	334	VSYHIEMSF FEVYNEKIHDLLVCKDENG QRKQPVRLKQFIICFEFLFL
11748	25649	A	11851	198	352	SRQGTWGIHGLECFVCLFVLFETESH FVPRLECSGAISAHCTLHLPGL
11749	25650	A	11852	371	1	PPKKLGIQVFTFPAPRAFWFVLVFKKKG FPQGNLVLPGFFSKVSIQGVPPFCRKPF SGWGEAFQIGFFINRGKFFFPPLGFFL KKVFLKFLAKFFFFFFFFFETESHVAQ AGVQWRSGLV
11750	25651	A	11853	176	3	KKGFPLDWNMVKNIIVKFGEDLQISKT LHTFFFLTESRSVAQAGMQWCDLGLSHS C
11751	25652	A	11854	281	375	QLTFKKYFLGWARWLTPVIPALWEAKAG RSP
11752	25653	A	11855	146	356	KCGALIAEIEVPLFSELDRDILLAYSMT ELCFKRCVPSLHHRALDAVDDCLHSCS CTDYPINRSLMNAY
11753	25654	A	11856	136	1	LSILCEFFNWLITEMEYRSVSQAGVQWCD LSSLKPPPPRLQOCHSC
11754	25655	A	11857	277	361	IVLRGAMWLTPVIPTLWRAEEGGSPEVR
11755	25656	A	11858	295	152	VVFGFGFFETESHFVAQPGVQWCDLGLS CSRLRPGSSNSPASAFQA
11756	25657	A	11859	1	342	GTRLPEPLTVLWTAHLGAMAPGSRISLL LAFALLCLPWLQEAQVAPVSRFLPDH AMLQAHRAHQLAIDTYQESEETIIPKDH KYSLLHDSQTCFRFSDSIPTPNMEDTQ HK
11757	25658	A	11860	244	332	TIEMMLDIKIQVIFLFEFKMGRKIAET T
11758	25659	A	11861	1	339	GTRVVTICQVLHAYAHFLYFFEMEARS VAQAGVRWCDLGLSQPPPPGSSSSSSSS S
11759	25660	A	11862	311	394	GMLGAVAHACNPSTLGGGLGGWITCSQEF
11760	25661	A	11863	130	1	VEPSVRTFFFFFFFFFETESRSVSQAGVQWH YLGLLQAPPPGSTSC
11761	25662	A	11864	3	320	IMMYALFLLSVGLVMGFVGFSSKPSPIY GGLVLIVSGVVGCVIILNFGGGYMGIV FLIYLGMMVVFYTTAMAIEEYPEAWG SGVEVLVSVLVGLAMEVGLVLW
11762	25663	A	11866	165	309	GLILLPMLECSDRISAHCSLYLLGSYDP SDSGSHVAGTTGTCHYAWLR
11763	25664	A	11867	208	314	GSRNKLSGQAQWLTPVIPALWEAEVGG PEIRSSR
11764	25665	A	11868	102	1	KKFFFFFFFFETESHVAQARVQCNLGSLQA PPPRFT
11765	25666	A	11869	126	3	NNALQLHSSYCKKPPFFFLKTESRSLTK AGVQWCDLGLLQ
11766	25667	A	11870	1	273	KQLPVNFLNWRLELTGLLCTLNLSKPC MIFIILVIVKYWFLFCNIFKNHIFSQA QWPTPVI PALWEADMGGSHGYWITTIVD FMCATLT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11767	25668	A	11871	126	2	FPKALLVVFFFFFFFFFETESRSVAQARVQWHNPGSLQCPLR
11768	25669	A	11873	269	9	QVSGKFWPDIFYKTGEKGLQCPNFPQGHPPRGLKKKSFSKKKKKKKKSIIVGQAQWLIPVIPALWEAKVGRSPEVKSSRPACTW
11769	25670	A	11874	114	1	LEAKPGVFQSGVLLVIFFFETESHVSQAGVRWCDLG
11770	25671	A	11875	146	1	GNHLSSRVGVQDQPRQHGKTLSLQKIQKVAGPGCAHLQSQEVQVGGSL
11771	25672	A	11876	2	159	SLQFFFFFFRWSFVLVAQAGVQWHDLGSQQPPPPGFKHSPASASQVAGRGR
11772	25673	A	11877	124	240	FRFSSGQAWLTPVIPALWEAETGGSLERSSRPDWR
11773	25674	A	11878	135	5	QVLFYFYFSDSFTLSPRLECSGVTLPHCNLCLPGSSDSCASAS
11774	25675	A	11879	170	2	GFFFFPEKWGYKNSFLCFFFFFFFEPEFCVSAQAGVQWLHLGSLQPPPPVFKVDAAP
11775	25676	A	11880	97	267	GHGHATLRGLCVLSLFFHIPAPSVSGTSDAECCLCVIYRLICGYISRNCLYFSDHR
11776	25677	A	11881	1	292	LPEPLRLVLTAAHLQAMAPRSRTTLLAFALLCLPWLQEAGADQTVPLSRLFDHAMLHAHRAHQLAIDTYQEFQTYIPEDQKYSFLHDSQTYFCFSD
11777	25678	A	11882	93	2	KYQMGWAWWLTPVILALWEAEAGRSPETSC
11778	25679	A	11883	145	2	PPLGLRLQVQAPTGFFFFFFFFETESRSPRLKCKGAILAHCNVCLLLV
11779	25680	A	11884	202	1	TWWRWGVTVLRLVMNCRPCDRHKSASQLIGRVRQENGLNARVGGCSEPRSRHCTPVWVTSENPSSC
11780	25681	A	11885	42	155	GERSGLSPGVQDEPGQHSQTSSLQKILKLAGHGGTCP
11781	25682	A	11886	215	1	STMARHCPLSPMLFNSAMEVLVRAISQEKIQGIQIGKEEVQLSLFTDDMIFNLEKRKDCSKNLLQLMNLV
11782	25683	A	11887	214	1	GYFFGLNEVLGKLEKPSLKVPQNPSPKRPFFLGFFFFETESRIVARLECSGAISAHFNLCLPGSSDSPVSC
11783	25684	A	11888	215	3	WGPGFPPFSFFFFFFLROGLAVIRLKCSGTITAHCSLNLGSSDPPASVSLVATTGHEPSITQFHSHGSC
11784	25685	A	11889	118	1	RFFIMGENPTKFFFFFFETESLLPRLECSGVISAHCNLS
11785	25686	A	11890	267	83	HCLRSGVQDQPGQHGKNPSIQKIQLATSFKKSLKIVIPPLPFKNDKTDSSKSSCLSPHS
11786	25687	A	11891	134	2	DRLAVLPRLECSGMIFLLPLPSRFKRFSCLSLPSSWDYRCAPRA
11787	25688	A	11892	116	1	SKGVGHFLFFFFFFETESRSVAKTGQVQWCDLGSLLCLV
11788	25689	A	11893	397	475	RFVCSTIKVLRDLSSDRSNPGRFLST
11789	25690	A	11894	115	331	KNVCLFVFMKNHLNPGDEGCKSPRSRHCTPSWAAQQDSISKYICIRYLYLDIYLSKLVRLRINQLPNS
11790	25691	A	11895	134	251	INPPVSRKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKGGGL
11791	25692	A	11896	186	402	PGKNLTLENVPRENKVGKAPGQNEPPV LGGGEYQDPGGNVKGVGPPAPGFGKDG PKRLADTFDLIEGDGD
11792	25693	A	11897	100	2	KGPPFFFFFFFFFFFFFFFFGQSGQVKLK SPKCK
11793	25694	A	11898	92	3	SVARIMPYALFLLSVGLVMGFVGFSSKPS
11794	25695	A	11899	283	362	MTYMTTIVHALWASVCLLLNHAHDPLD
11795	25696	A	11900	248	1	VMSAQPGLSVILRFMGKWSNWTGMQYTE SEVERYDRGRARETERQRDRERENP RNRKLFFYGRFKHSPQDFMPQKVHF
11796	25697	A	11901	253	2	KLQENPFKLLNFIINLCSVSLNVPTILN INIKPSFIAPKPRCPSKFQRYIYIYPS IYLSIYLSIYLSIYLPITISKVLKDVE
11797	25698	A	11902	179	3	LAVTKNEIMGFSTIWMEMGDINFFFFFF ETKSHPMRLECSGVISAHCNLRILVSS SC
11798	25699	A	11903	1	403	GTSSQESFGGCCVSGLIAMGTAKQGERK LLCLFILAILLCSLALGSVTVHSSEPEV IIPENNPVKLICAFYDLFFFSSFSYFF HLSFFIYYPYLFVSCFTFYIVILLSFI YSHHLSVSYSYVLLIYTFIL
11799	25700	A	11904	37	242	KGPTRDQLQHPKARLPAPLRVLWTAHLA AMAAGSRTSLLALFALLCLPWLIDGAS HIVSLFMLFIIF
11800	25701	A	11905	1	298	GTSQHRGRKDSRTGSHSSSDHPGAKLLS TEEKQAAETMRPPSAPPRRGCI PWQGLL LSSS
11801	25702	A	11906	225	30	ACYLQKDGAFAILPDVLPDMFKGHSSLY PCQHAECDHIKNIYNCVCVCVCVCVC IVICKLNV
11802	25703	A	11907	196	320	HSSSSTTPSQDTHTHTHTHTHTHTHTH HKIPQRELLPSVPD
11803	25704	A	11908	130	3	NGFVFSPFFFFFFFEMESHSVTQARVQW CDLGSLSLPPGFK
11804	25705	A	11909	381	2	ASTCGQLTFQHWKKIILVQQVGLQKK NSTLKRAWEFLSFFQAPPLGSPKGIN ILNKGAKLKGKTNFGPIVFFFSVLPP FFGLKKFQKKVFHQKSPFFFFFFFETE SRVAQAGVQWHD
11805	25706	A	11910	138	2	SVPLKEFIISQARWLTIIPALWEAEAG RSPEVRSSRPASTWRNP
11806	25707	A	11911	231	54	IRASFGIQRICLTIFFFETEPHSVTQ AGVQWRDLGSLQPPPRRQEQNSVSKQTK TN
11807	25708	A	11912	3	461	DAWGRVEGPPLRPPATSRWAGPTLWRM EVTGDAGVPESGEIRTLKPCLLRRNYSR EQHGVAVSCLEDLRSKACDILADKSLT PVTLVLAEDGTIVDDDDYFLCLPSNTKF VAMAINERWAYNNNGGTGWISQESFDV FEAYSGATLLFFF
11808	25709	A	11913	318	407	LCGRLLWMLPVIIPALWEAEAGLLKLR MR
11809	25710	A	11914	340	5	DRVAKFSEARLFRLLFFFFFLKIFCFPR GFKIFRGVCPLLPPEFWGLFQKGPGR LFFPPLGGFFFFFFFFFFFFFFFFFFFF FFPFFFFFFFFFCHKNTLLKKVHNSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11810	25711	A	11915	274	385	IKPQRWGETRAEKLKSLKIRVPLLLQRN AAPHQQWNK
11811	25712	A	11916	259	441	DTKLPKVNLIKLNPHALKKKKKKKKKKKK KKKKKKKKSSSLRG
11812	25713	A	11917	254	402	LIVSVIDFLRWRLPLLPKLECSGMISAH CRLRLPGSYHSPASGCQLLGR
11813	25714	A	11918	223	1	NTNSPRKKFFYEVSVPVFFGVFPSP LKGSPRAFLKLAWRPPLPLFFFLEMSR SAAQPEVQWCDLGLSLQPP
11814	25715	A	11919	97	3	KPFFFPFFFFFEIESRSVTQAGVQWRD LGS
11815	25716	A	11920	154	384	KEFFLMLFFFLPPPPPPFFFLGKGLF FFPPGGGGGGQFFSIGPPPPRGKDEPP SPPKMGGRGTTPPPGYFFFF
11816	25717	A	11921	225	369	GTLNLLTYKIKSWGAVAHYNPSTLGGW GKWITSGQEFETSLANVVKP
11817	25718	A	11922	116	372	MEYTNKMMASYNLHIYQTYKNSVIEHP TGVLPHSRVIMVNNIVLCISKQLKELLR RLMWEEHLSPPGGGCGSEPRSRHCTPAWA T
11818	25719	A	11923	271	409	KKKKKKKKKKKKKKKKKKKTGGGA
11819	25720	A	11924	121	228	KKKKKKKKKKKKKKKKKKKKKKKKKKR GGGFKKKPWGGQK
11820	25721	A	11925	55	423	NKPKKKNFKKKKKNFFFPYPLKFFFF PKSLNFFRRVVPKISPPKKKFFFKNSPS VFFFPPLKKKNFFFLTPLKFGPPKNFFK RPPPLFFFFFFFFFSLGNCIEKL
11821	25722	A	11926	253	443	YQHQRPKVDKSMKGRNQRKKSENSKNQ NTSSPPKDHNSSPARQQNWMENEFDLT EVGFRRW
11822	25723	A	11928	175	413	KKKKKKKKKKKKKKKKKKKKKAGGG A
11823	25724	A	11929	490	182	RKQKIKGCKKPNPLAQGGVKKKKGKGP FNFFLKQKGQDFLKNWNLGQKKKIPIPP QVFSLRQKGAFPGRIFFFFFFFFETESCS VAQAGVQTLKYKNKNKIK
11824	25725	A	11930	110	2	KKIPRKPPFFFFFFFFFYKAGSHLVAQAG VQWHDLS
11825	25726	A	11931	169	987	YLEKIMSEHSRNSDQEELLDEEINEDEI LANLSAEELKELQSEMEVAPDPSLPVG MIQKDQTDKPPTGNFNHKS LVDYMYWEK ASRRMLEEERVVPTFKSEEKTQEEHBE IEKRNKNMAQYLKEKLNNEIVANKRESK GSSNIQETDEEDEDEEDDDDEGEDDG EESSETNREEEGKAKEQIRNCENNCQQV TDKAFKEQRDRPEAQEQSEKKISKLDPK KLALDTSFLKVSTRPSGNQTDLDGSLRR VRKNDPDMKELNLNINENIRK
11826	25727	A	11932	161	389	SVQTHPNLRSCSVLKNAMHFYLLGYVIS GCTEPAKAIKPIDRKSVHQCISGPVVL LSTAVKKIVGNSLDAGATNI
11827	25728	A	11933	134	289	ASTQNMGMRLRLMSSPTLLSLSLSHTHI HKHTRMHTHTHTHTHTYPTTKV
11828	25729	A	11934	128	1	IKKGEFFFFFFFFFETESHSPRLQCSGTI LAHCNLHLLGSSNS
11829	25730	A	11935	131	19	MYIGWVQWLTPVIPALWEPKVGASLEAR SLRPARTSE
11830	25731	A	11936	104	3	LKGQLIRAQWLMPVIPSLWEAEMGRSPE

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						VGSSR
11831	25732	A	11937	146	2	GGRLGIITYHAWNPEGFFFFFEMESCSVG QAGVQWCNLSLQPPHPGFK
11832	25733	A	11938	149	1	DKCFLCVCLFIFITYLLIYFYFFETESC SIAQAGVQCCNLGSPQPLPLA
11833	25734	A	11940	176	380	QSVQQLPRLECNGMILAHCSLHLLGFKR FSCLSLPSSWDYSRLRNYQGGRRWSKTH QAWCQSLTILWN
11834	25735	A	11941	133	415	KKKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKSG
11835	25736	A	11942	222	420	QGDKFLDNNNSTILYMEKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKYSR
11836	25737	A	11943	163	425	KNPPKNSQLSPSTLKKKKKKKKKKKKKK KKKKKKKKKKKKKKKTG
11837	25738	A	11944	143	3	KMGKKQSRKTGNSKKQSASPPPKERSSS PAMEQSWTENDFDELREE
11838	25739	A	11945	200	3	QNSQVGYKGAPHKEKTMALQARVNLGPP RGPLKRPALFFFFFETESPSVTQDGVQW HDLGSMQPP
11839	25740	A	11946	221	3	RKIEGGPSTSRKSVRGVRCFQPLGLGFP GGLFFFFFFYETESCSVARLECSGVVSA HCILHLRSTNEGRRGR
11840	25741	A	11947	68	177	ISSSFKNKCLCEKKKKKKKKKKKKKKKK KKKKKKRK
11841	25742	A	11948	210	329	RHTHTHTHTHTHILSLSLSHHTHTAHTL MYFLAFFDLRS
11842	25743	A	11949	183	20	LGTVAHSCNFVFSLSRGLHVGNGLRL PTSDDPPTSASQSAGTGMSPCTWPE
11843	25744	A	11950	232	329	VGIKMSISSDEVNFLVRYLQESGFSSHS AFTF
11844	25745	A	11951	412	239	LFYEKGSRFVSQAGLELLELKQSPCFGL PKCWDYRHEPPRQADLPFCVPSSAWASW L
11845	25746	A	11952	310	393	PHTDISGTPEIMHYVHVHRTVTPQPNKP
11846	25747	A	11953	193	3	LSSWPTLISGAFKAENAVEGNDDSRIL RGFFVLFCFVLFRRQSLALSPRLECSGV ISAHCNL
11847	25748	A	11954	185	416	SVQTHPNLRSCSVLKNAMHYLLGTEPA KAIKPIDRKSVHQICSGPVVLSLSTAVK KIVGNSLDAGATNIDLKLDY
11848	25749	A	11955	100	1	AHLSKVFPFFFFFFFEMESHVTRLECSG TISAH
11849	25750	A	11956	35	521	KEKFFFHAGVYWGPPRNFLKRAPLFFFF FFFFFFFFFFFFSFFFS
11850	25751	A	11957	214	1	KKKIFFFKEIFYPKLSRKKKNFRGAGK ILNLSIFPEKKKIFSPSFFFTESCTV AQAGVQWHVLGSLQP
11851	25752	A	11958	114	1	RYFSGQAQWLTPVIPALWEAEAGRSPEV SSSRPAWLTV
11852	25753	A	11959	188	12	SKCQCTFFSNFKKTEMESHYLAQAGLEL LGFSHLPTSVSQTVGITGVSHCAQPNH LY
11853	25754	A	11960	241	556	SSIPFLPNKHLLLSFSTLSSLGREVSIG DMCQGTQKQFPFPLPHVFLSIRDGE LCVGRDVHLTCQTDLAQVFCVFLVGLVL LSLPRAGVQWCHLSSSQPPPP
11854	25755	A	11962	362	462	KIGQALTPIIPLLWEAEAGASPEARSSR

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						SAWPT
11855	25756	A	11963	43	2	CCCYCCCCCYCC
11856	25757	A	11964	30	415	GLGFKQKIFFFFLGQGPNFLLRAKKR PFLPPPPFPKNPKNRGVFLGPGSVKPK RPRQGDVPLKPRSLGVFLTSKKTPLGP WANPPPPPGDGP
11857	25758	A	11965	149	2	SKTWLKLAKYLKNTYPGWVRWLIPVPA LWQAGAGELHEPRNLRPAWAT
11858	25759	A	11966	179	3	KKNIFPPPPVKFGPPQGFFKRPPPLFFF FFFFFFFETESRSVAQAGVQWLSIGSLQ AP
11859	25760	A	11967	245	382	DVTDSKMHDPDRSSHVKMWLGVAHACN PSTLGGSRGQEFKTSAN
11860	25761	A	11968	264	10	LSTLECKGVSPGVFSPKGRKGLGYIFS PFLEKPHPLPLGISMYFFFFFDGVSVAQ AGVQGRDLGSLHLPSPGSSSYSCASASLS S
11861	25762	A	11969	326	406	RLLKGWALWLTVPVITLWEATVGRSPE
11862	25763	A	11970	120	1	KGYGFPFPKPLGPPFFFFFATESCSV AQDGVQWRDLGS
11863	25764	A	11971	84	370	RNGAELKTPLAGQTQITINCRYSWVTLV LGDLESILCWHIFKKTNLFCGFFSSFL LGAGRMKSHCVVRLECRGMISAHRNVCL LGSNDSPCSAF
11864	25765	A	11972	196	3	SRGKMGEYFPVLFKNPSWAKAGGNKGNP FFFFFEAESCSVAQAAVQWCNLGSLQAP PPRFTPRA
11865	25766	A	11973	559	644	KIGCSAYGVAILLFLYFFNKLAFTLWKK
11866	25767	A	11974	3	391	HEAQLPEPLMVLGTGHLAEMAGGSRTYL LLAFGLLCLPWLQEAQAQTVPLSRLFD HAMLQAHRAHQLAIDTYQELEETIYPKD QKHSFLHDSQTSFCLSDSIPTPSNMEET QQKSNLELLRISLLLE
11867	25768	A	11975	138	365	LKFECHSTLCANHGKQTFTFVFNKFL KYTFYFVSLTYAINWYIKNLINVFKKKK KKKKKKKKKKKNFKKKKN
11868	25769	A	11976	275	433	MSILDLSKARNFFLSFLETGSCSITQAG VQWLNHSSLQPQTPGLRDPASASQ
11869	25770	A	11977	108	3	RCGLFFPETRASPCRPGWHNLGSLQPLP PRFKRF
11870	25771	A	11978	270	408	FENNVWLGRAQWLTPVIPALWEAQAGRS PGPENQNHDPYKGNPWPY
11871	25772	A	11979	228	441	QALKFVTEMLLSLKKCLDVSVIFNRHKK IELLQKKKKKKKKKKKKKKPSQKKKD SSRGKDS
11872	25773	A	11980	2	447	GALALNKTADVWRLNFLVSGLHWKRWL QOTSLSKWKIKECSILKKKKKKKKKK KKKKKKKKDKK
11873	25774	A	11981	124	445	KYGEMSQNPARGGPKFSKNQKYSEHLRI HCCPPFTFLISKKEIGDRKYSICKSGCF YQKKEEDWFCPCQKTKTSRRAKSLKRP KQKPVAPPGGVKAPAKPRSLPRF
11874	25775	A	11982	48	429	KESNGSQDRLLPKIHSPDVSGGKSGGMS QNPARGGPKLSKNQKSEHLRIHCCPPL PFLISKKEIGDRKYSFGKSGCFQKKKE DWICCPCKTKLKGKIRPPPKKNGPGGS LNGRTTWVSGLFVHN

[illegible]

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKPFPCQVGLILAPFRVLLIGRPFFFFF GVLVVEIQRWSFISLVVVVRARIMMYA LFLLSVGLVMGFVEFSSKHCPVYGALVL VSIIGRV
11898	25799	A	12006	189	12	DGRLPGSVCCYLIIFLRQSFTLLAQAGAQ WCHLGSLSQPPPGFKRRVSRIRAVRG DQ
11899	25800	A	12007	131	3	KIFFFFFFFFEMESHVAQAGVQWRDLGS MQDPPPGFMPLLFY
11900	25801	A	12008	150	2	IILFLVPIEAVFFFFFFETVAEAGVQWHNL SSLQPPPPGFKQSPASARVA
11901	25802	A	12009	305	3	KFFSLKASIRGRWFGLEFTTPPKGFLP KIPHOVFKGGPLWEKLQLGKAGLNLGPY KGFFKGAARFFFFFFETESRSVAQAGVQ WRDLAHASVHASAHAS
11902	25803	A	12010	263	517	DKGFQLPPRWCPGQDPLFFYGGIVFHGG YGPFFFFFFFKAESRLVAQAGVQWQDLG SLQPPPCRTRGSP
11903	25804	A	12011	107	374	WMGTWGSLEPVLITRSTCPPRSPRLHRR TGATIWIIFRLEFETGTVLPMLECSVIM AHCRLQLPGSSSSPTIASQVAGTKAHL DCFVY
11904	25805	A	12012	144	261	FPKINNFFYFTFLQDPTGIFSLDKTIGL GTYGRIYLV
11905	25806	A	12013	371	3	IFHLRKIFTFLPGIFWPRIILSEKKPK RFVVKIKKFKNGYPLKNPINPKYKGRPF FFKGEKNPNKGVPVLKKIKIPSFSKALG FLQKKASKPFFFFFFDTECTVDQSGVQ WCDLGSQAP
11906	25807	A	12014	101	3	RGAFFFFFFFFETRSRSVIQAGVQWCDLGS LQAP
11907	25808	A	12015	205	2	VFNPSGINVMYVDATILNKRLATRIQQH IKQRILHDQVGFHGMQGWFSIRKSINV IQHINRPKDKN
11908	25809	A	12016	168	1	GCVCQFQKKLGNGLNGFFFPFFFFFF EMKRSRVVQAGVHWRYLSSLQTPPEFK RGLRFGQWKTQMNPNTPFSALRPGQLS SIRSGLLHTYPGLGDRSEPLSCSILSSS KYVVWQAVTSALSSNKPQASQGHWKDDF FLFFETESCSVTQAGVQWH
11910	25811	A	12018	383	247	LVEMGFRHVQDGLDLTSSQSAHLGLPK WWDYRREPRLATIEVL
11911	25812	A	12019	2	379	RVLWTAHLAAMAAGSRTSLLLAFAALLCL PWLQEAGAVQTVPLSRLEKEAMLQAHRA HQLAIDTYQEFISSWGMEAYITKEQKYS FLHDSQTSFCFSDSIPTSSNMEETQQKS NLELLHISLLIES
11912	25813	A	12020	3	389	PEPLRVLWTAHRGAKGAGSRTSLLLGFA LLCLPWLQEAGAVQTVPLSKLFDHAMLQ AHRAHQLAIDTYQEFETYIIPEDQKYSF LHDSQTSFCFSDSIPTSPNMEETQQKTN LELLRIFLVLELWLDLP
11913	25814	A	12021	247	386	PMLGHVSQSGNGVRDPLEEAVCPPLAKL KHCSGRSTALFRAGRQKR
11914	25815	A	12022	17	371	PLRDLWTAHLEAMAPSFRTDLLLAYALL CLPWLQEARAVQTVSLYRLSDHAMLQAH RAHQLAIDTYHEIETYILKDQKYSFLH DSQTSFCFSDSIPTSPNKEETQQKPYLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLPISL
11915	25816	A	12023	3	359	LRALWTADLGAKAPGSRFTLLLASALLC LPWLEEAGAGQTVPLSKLFDHAILQHR AHQLAIDTYQELEETYPKDKHSLD SQTSCFLDSIPTPSNMEETROKSNLEL FRTSLLL
11916	25817	A	12024	2	363	PEPLKGLWTDHLGALAPSSRTSLLLAYA LLCLPWLQEAGAGQTVPVYTLFDHAMLQ AHRAHQLAIDTYHELDETYMPEDHKYSF LHDSQTCFCFSDSITTPYNMEETQHTSN VELLRISL
11917	25818	A	12025	314	393	GQAWWLTPVIPAFWEAKGGRSLEARS
11918	25819	A	12026	80	392	PLIACSFLLFLFFFGKKILFLPPRWKG GGGIWVNGNPGFRGQAFFLASSSKKPGM GGPPLTPGKRFFVLKKGFSPGGPGGSK FSAPGTPPTGPPKGWEIPAK
11919	25820	A	12027	165	2	WQKLLFHFGTESCSVARVGVQRHFSFP KPPPEPFKQLSAPASRVADRRPPDAW
11920	25821	A	12028	1	338	VFVALKFLMCLLSVCFSLNENIYNSLP QKNCLPLIFFFLFFEMEACSVTQAGVQW GDLGSLQPPVSHLNLGGGCGCEPRECHC TPCSRPGDRDFVFNKNTMIQDNHLMELT
11921	25822	A	12029	2	315	HEERERERERERERERERERVRGTVC GVGETYKAELPRVGGAAQKRAHFSARGR LFMEICGDMCGEKGKPPHSLTECLSR CGERFFDTSLAITRGCAQSV
11922	25823	A	12030	216	3	ERIIPRGVRQRNRLFSGRDTASPLFPY PPRQIHKRGVEDREHRRGERERERERE RERERERERARAAR
11923	25824	A	12031	114	329	QTERNSTININKKDIHTKTPSVGHQHRP KVDKTTKMGRNQSRKAENSKNWKASSPP KEHNSSPAREQNWMES
11924	25825	A	12032	177	1	IKKKTFFWQNIPLFSKKKTCRQKFFFFF FFETGSLPLRLVCSGAVLAHCSLCLPGS AFL
11925	25826	A	12033	127	1	PSFFFFFFFNETESRSVAQAGVQWRDL SLQAPPPGFITPSC
11926	25827	A	12034	47	314	GAPVASVSISCPSCSATDGVVRNGKSTA GHQRYLCSHCRKTWQLQFTYTASQPGTH QKIIDMAMNGVGCRTARIMGVGLNTIL RHLKN
11927	25828	A	12035	15	408	GAIPGAMGHFTEEDKATITSLWGMVNAE DAGGETLERLLVDYPWTQRFFDSFGNLS SASAIMGNPKVMAHGKVLTSLGDATAKH LDDLKGTFAQLSELHCDKLHVDPENFKL LGNVLVTGMAIHLGKEFTP
11928	25829	A	12036	122	2	KLVDVLPPPGGARVFFFFFFFPLETEHCS VAKAGVQWHDG
11929	25830	A	12037	154	1	GKPPPKLGFWGGPRQVRGRGPPFFFFFF ETESPSVAKAGVQWCDLGSLLHPL
11930	25831	A	12038	58	254	DPRVRQQRRTAHCSLNLPLGQRPPSLSL PSGWDYRHAPLCATQKILAYRVAQRERS AHGSYYQAS
11931	25832	A	12039	270	124	DGVLLLLPRLECNCAISAHGNLRLPGSS NSPASNKTQNNNKKTLNKF
11932	25833	A	12040	63	355	LGRGTAHRLWRPLSRPASRVSYLSAAT NKRSEAPPSPAFPDNKNWGGFFYFFET GSHRRRPGRMECSGAITAHCSLDFPGSE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MGFTMFPSLVNS
11933	25834	A	12041	184	3	GVSRLGGVSQLGYMGVRDPLEEAVCLF SKLKHHPGRTTALFRAVRQGCLSLQKFL LLFA
11934	25835	A	12042	118	3	DRVLLCYLGWECSGTISAYCNLHLPKSK RFSCLSLPSS
11935	25836	A	12043	40	436	LSEGKLTNRKDNHTKTPSVHHHQKPKV DKTTRMGRIQSTKAENSKNESTSSPPKE HSTSPATEQSRMENDFDELREDFRRSVI TNFSELKEDVRTLCCKEAKNLEKRLDEWR TRINSMEKTINDLMELKMA
11936	25837	A	12044	101	2	HLGQVRWLTVPVIPILWEAEVGGSPPEHRS SRPAW
11937	25838	A	12045	123	3	LTVIKELPLGQARWLTVPVIALWEVKVG GSEVRSSRPA
11938	25839	A	12046	3	432	PIFGGGERIFPFFFFFFSQGGGVFFPKT KNKGFFPFLGFFKKIFLRNFFFLFFPFF FLNPFYFGAPPPFFFGGGFFFLFS RFFKFFQNFPGFFFGGGFFFLGFF FFFFFL
11939	25840	A	12047	325	164	KNKRKNRGQARWLTVPVIALWEAEAGGS PEVRTTGVSHGTRPHLLNTVSEYI
11940	25841	A	12048	187	381	LMDKRVSLWGDENILKVESNSGCTTLYL LVCFEMESRSITQAGVQWRDLSSLQPPP SRFKRFSC
11941	25842	A	12049	84	464	SYRVPSHPDTLVLSRISAQEAAGEKSPFC FPERVWPCPRPLSDLGRRLKLECGPDL DSTFLSFFEGGLKTGSHSGALECSGVI RDHCGCLCSGSGDPPISACLVRAGTTGV SHHCIFCRQDLPGS
11942	25843	A	12050	232	20	LLQCSSRAKIHTSLTGNQKLEMIKLSEE GMSKAEISQKLGLLHHLGLVANAKORFL KVIRSATPEFRHAE
11943	25844	A	12051	401	518	FFETESCSVTQAGVQWRNLSPLRA
11944	25845	A	12052	191	1	LFPLKKEKILFLGPGTNGAPPMFFLKAP PLFFFFFFFVFNLFLL LSFLHILEP
11945	25846	A	12053	12	369	PLPIYSACIEVGSNPQPGIDAKSVSHN NCYLKEKKKKSNGSQNNLLPKIHTPENG SGKKTGEKIQNPPRGGPKLSKNQKYSKN LKKHCCPRLTFLISKREKGNRKYTFGKS GCFYQKK
11946	25847	A	12054	89	513	NFTVRGSIPLNNIPMANLLLLIVPILI AMAFMLTERKILGYIQLRKGPNVVGPI GLLQPFADAIPLFPKEPLTPAPSALC FAAPALALPFALFLCPRPLGRP
11947	25848	A	12055	158	3	SQLTWPIMAQTDMSCLWIVYFDDNIGWA WWLMSVPTLWEAKVGGSLHNS
11948	25849	A	12056	113	1	KSHGGHGVFVLVSVLVGLAMEVGLVLVW KEYDGAALA
11949	25850	A	12057	44	263	ARIARSAHEGKMPRKYTGARKNAENRPO RELQLKASRSTIDLAHACNALWYQLFL ISVGSWKNYILFYLTYY
11950	25851	A	12058	142	1	KKIFFRYKKEGFSFPKFRISLFFFFFF ETESRSVAQAGVQWRDLGS
11951	25852	A	12059	12	347	QTERNSININKDIHTETPSEGHQHQRP IVDKSTKMRKNQCKKAENSKQSASSPA KDHNCPLPAKEQNWTEFHKLTVEGFRI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITNSVELKEHILTQCKEAKNLEQRLEEL
11952	25853	A	12060	245	3	MPEGSFFLEIPEITRVFVKPGKFLGGV GPSLLFFFPFFFFFFFMRQSLAVSPRLEC NSAISAHCNLCLLGSSDSRSSGSR
11953	25854	A	12061	94	3	KGGIFFFFFFFFLQSPSPVAQAGVQWCD LG
11954	25855	A	12062	108	5	NNLSSGVRDQPGQHGETTSLKIQKLAR HGGRHL
11955	25856	A	12063	298	1	KKKKINTHAQKRGPPFFFKPPPEKGKAP PPQRVTKKGGEKDSFIPKRREKKNPPPL SFFFLVLRVHVRERERARERERERERER ERERERERERERERERAR
11956	25857	A	12064	122	1	VCEGVCVGGWVRDRERERERERERERER ERERERERERAR
11957	25858	A	12065	126	1	ATCTKFRNDNRALLRVRFERERERERE RERERERERERERESR
11958	25859	A	12066	48	351	FFFFFFFFKKGPKIVPPGGGGGGDPIFL EPPPPPLKKFWGPPLRGRNKGGGPPGW VNFGIFLKKKGLPWGPGGVKTPAFKGS GPTPPKGGNNRKNPPPW
11959	25860	A	12067	1	365	GTRLTVLWTAHLVAMAPGSRSTSLLDFA LLCLPWLQEAGAVQTVPLSRLFDHAMLQ AHRAHQLGIDTYQEDEETYIPKDHEDSF LHDCQTSFCFSDSIPTPSNMEETRQKYH LELLRISLLF
11960	25861	A	12068	174	1	PAWVMQHNVPVSLFFCFETESRSLTRLE CSGTISAHCNVRLLPGSSDSPVSPSRVAA RA
11961	25862	A	12069	270	375	TRIKRCNGGRAQWLTPVIPALWEAKAGE SPEVRSS
11962	25863	A	12070	197	350	KKIYIFLTINTIMDLIIPFLDNILGFW LGAVAHACNPSTLGGRGCWITRS
11963	25864	A	12071	3	378	HEGQLPEPLKGLWTAHLGMAPGSRSTSL LLAIDLCLPWLKEAVAVQTVPLSRLYD HAMLQAHRAHQLAIDTYQBIETTYIPKD QKLSFLHEYQTSFCFSDSIPTPSNMEET LHKSHLELLRIYL
11964	25865	A	12072	219	1	FSHPFPFPGVFTPLVFPRPWEVLGSPGG GGGPPKKWAGVQKWVFFFFFFFWEMESC SVAQAGVQWYDLGSPRA
11965	25866	A	12073	134	3	VFGPPFFFFFFCETESHSAQAGVQWRD LCSLQAPPPGFMPS
11966	25867	A	12074	175	357	MPINQPVKKMCVCVCVYIYIHTPLYI RVYMYMCMYICVYIHVYIWMCIYIHTHV STYVW
11967	25868	A	12075	193	350	KIPHLTSLYHTQNYLKYCIGQAWWLTPV IPALWEAEAGGSPEVRSSRPAPWP
11968	25869	A	12076	252	1	GVFGFPFKKGGFFWVKGLGTPQIFWVG VFVKKKGGALWVKGLLGKPPPPPLFFFF FETESCSVARAGVQWRDSVKKKITARA
11969	25870	A	12077	273	366	IFIYLFYLFETESCSVSQAGVQWPNLG RLR
11970	25871	A	12078	127	2	KKKKTLFFFFFFFEMESRSVTQAGVQW CDLSSLQPPPLV
11971	25872	A	12079	206	334	HNRVTIVNNLIVHFKITKRCWTQWLTP VIPALWEAKAGGSSE
11972	25873	A	12080	135	2	KMKRKFGEQSQIPKTLQTFFFLTESRSV AQAGMQWCDLGLSHSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11973	25874	A	12081	147	3	ATTPGLFFIFYYFFETESHSAQAGVQCM ISVHCNLCCLPGSSDSPVLV
11974	25875	A	12082	106	2	YFIPINEGYCFIYLFFETESRSVVQAGV QWCDLV
11975	25876	A	12083	164	346	CPYKKRKKKANQAKWLTPVIMLFGRRRV DRPSSGVQDKPGQHGETPSLPKIQKKSQ AWWCA
11976	25877	A	12084	186	1	KSLFSKGNNPLFKGPPPPPPPPPPPPFETR SRSVTQAGWGAVIMAHCCNLNLGPSPDPP TPAPRA
11977	25878	A	12085	98	2	CPFFRVNFFFFEMESRSVAQAGVQWRDL GSRA
11978	25879	A	12086	154	2	SPTPEKGVWELPSPFFSWGPKIWGCIFF FLYETESGSVAQAGVQWRDLGS
11979	25880	A	12087	326	3	KTSVITCGLPMGWSWGPFPPKGPWWCKKF CVCKFWANQTLKKNLGAGRFOKDFSA AA FLEMGGFPFKFFRFQGSQFFFFFFFET ECSVTQAGGWCNLGSRLPLPP
11980	25881	A	12088	154	3	KEFSFFAPGGKQRGEIRSLRGPPPQVKP LFFFFFFETESRSVAQAGVQWR
11981	25882	A	12089	174	2	SWKAILQYSLEIILYLPSFQIFLCFSHT HHTHTHTHTHTLYSQIMVLLLP SLRK KS
11982	25883	A	12090	265	30	WFIVYSEISQLWGLPSFNTLTGTQSLSF IFVAMRSCCVTQAGLELLASSDEPVSA S QSARIRAMSPSAVVIPIGRSR
11983	25884	A	12091	257	1	GSMVMHTEEQYPENKVEQSSSGFIRPH LVYRVCFYLSVCLSVCLSIYLSIYLSIY LSFFLSFFLLRKSILYSIFLSFFLLSPR V
11984	25885	A	12092	311	404	LYHQNPWLYSVFFFLETESCSVAQAGVQ WCD
11985	25886	A	12093	331	83	GDDYKGARENSRDDKLIFYVLIMMVVIQL HVFKIKHTLQLNGYILLCKLYLINLTK NNFQPKPKINSQKTLHIHPDSTAANI
11986	25887	A	12094	82	2	LREPNNLNPGGEGCNEARWCHCTPAL
11987	25888	A	12095	255	393	HGILFSSFVCNLSNQFLSQHWLMFPVIPAL WEAEVGGSLEPRSTLAW
11988	25889	A	12096	80	3	PPFFFFFFFFFFETESRSVARLECSGMI
11989	25890	A	12097	367	1	PRVDKPTKMGGKQGRKTNSKKQSPSAP PKERS SSPATEQSWMENDFAKLREEGFR RSNYSELQEEIIQTGKEVETFEKNLDEC ITRIPTNEKCLKELMELKPKAQELREEC RSLRSRCDQL
11990	25891	A	12098	94	236	MWADYFCMSPSID EGLKKKKKKKKKKKK KKKKKKKKKKKKKKKKGGAP
11991	25892	A	12099	410	212	NSLHPSTSLFRFSSHFIKLISGQAOWL TPIIPVPWEAKAGGLLETRSSRLAWAQ EDPISM PVCK
11992	25893	A	12100	140	324	NLGAQOWLMPVIPARPWEAEVGRSLAVR SSSNSPASASQSAGPTGPSHHNWMFLQ LLTRL
11993	25894	A	12101	247	357	KQIQGRAWWLTPVFSPLWEAKAGESPEV RSLRPAPWT
11994	25895	A	12102	245	2	DVLVGGCLCLPAGGTLHLTSIFLLSGCWC GSKDEEAPCKQRISVQRESQSRTLRAGV SPKKAHPCEMCGLILEDLVLFHPDLQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
11995	25896	A	12103	230	379	KEASFFETESHVSQAGVQWRSLNPLGS GNPPTSTSRVAGTTGMSHHVWL
11996	25897	A	12104	86	2	DGVSVLSRPLECNGLILAHCNRLPLGSS
11997	25898	A	12105	116	2	SQKTPFFFFFETVSLLLPKLECNCAISAH CNLCPLGSSD
11998	25899	A	12106	271	416	QFTFSKAFNLVFIKPSFHISFYRTHYSQ AWWLTPVIPELWEAEAGGSP
11999	25900	A	12107	194	3	HVLGTVLVAEDTASNKIRSLQGCLLLPL LFSVLEVLARAIRQEKEIKVIQIGRBE VNRRRGR
12000	25901	A	12108	142	3	LCLLYWDCKRHAWWRGQVRWLTPVIPAL WEAEAGGSPEVRSRLPAW
12001	25902	A	12109	233	346	HQRSLIGWAQWLMPVIPALWEAEAGVSP EVRSLKPAWP
12002	25903	A	12110	234	349	GFSPFYDFCLFVFETESCCVVQAGVRWH DLGSLQPPPP
12003	25904	A	12111	136	333	RLNFFFYFYFFETASCSVAQAGVQWHDLA HCIPAWETEQDSISKNTVQKRKKKVTRA GISKTKNENF
12004	25905	A	12112	345	110	QDGLCLVMTLQETQPILAYSLWFFIVFP TTKACNVQGDSKFLKKKYLGGVQWLMP VIPTLWGADVEGSPELRSLEPA
12005	25906	A	12113	108	285	YNAMKNRFLKTIILNNKNSIGWARWMAV IPALWEAKAGRSPEVKSSRSRPGAVAQV DAA
12006	25907	A	12114	1	364	RVVAAEMGKFMKPGKAALDLAGRYSGRK AVIVKNIDDGTSRDPYSHALVAGIDRYP RKETAAMGKKKIAKRSKIKSFVKVHNYH QLMPTRYSDIPLDKTVVNKDVFRDPAL KRKARREAK
12007	25908	A	12115	120	3	TQIWGAFLTLFFFFFFFEAKSHSVAQAGV QWCSLGLSLQA
12008	25909	A	12116	120	3	TQIWGPFLTFFFFFFFEAKSHSVAQAGV QWCSLGLSLQA
12009	25910	A	12117	231	1	FLSPFSCYSATTKLLSLSYFLLGHILL LGSTPEAAAQVVQWVSFADSDIVPPAST WVFPTLGLMHHNKQATENAKE
12010	25911	A	12118	216	1	LIFPPLLNFCYGEVLGFQGFALFFACM FFWPRFSPKTTTTFFYEKEFHSAQAQGV QWCDLGLSLQPLPRGFK
12011	25912	A	12120	267	1	KKKKKAFPSPLLGCFFIRLQKHLGLILV YRSHLISSLLCLEGIILSLFIIATLITL NTHSLLANIVPIAILVFAACEAAVGLAL LVSIS
12012	25913	A	12121	167	372	ISGQDLLKETKRVKRPQDDVPFINIF VPTPGAPRSLRQILELRGKTDPSPIIIVG DFNTLFSALDRS
12013	25914	A	12122	124	2	GLLKFNIFAPFFFFFFSETESHVSVAQGV QWCDLGLSLQPPPP
12014	25915	A	12123	121	1	RFTAASANSAGAVSAAGVGMGDPGSEIIE SVPPAGPVSSV
12015	25916	A	12124	176	2	RDLRGFSRFSNYKFWNFRVGGIFKFVF GKGVKRFFFFFFFETESCSVAQAGQWRD LG
12016	25917	A	12125	137	2	KLGFFGGGGGKIFAPQKNFFFFFFFFFEE MESCSVAQAGVQWRDIG
12017	25918	A	12126	103	3	LEENLGNTIQDIGRGKDFTSKTPKAMAT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KAKID
12018	25919	A	12127	212	351	LITFEILNLCIGDNLDLGLARWLTPVI PALWEAKAGGSPEVRSRLR
12019	25920	A	12129	187	3	RGSTMQQTNTRTPGVRVLYIYILMIATMA IPYIPMANLLLLIVPILIAMAFIMLTER KILGY
12020	25921	A	12130	13	329	ASRVITIRVMASNSTKSFLADAGYGEQEL DANSALMELDKGLRSGKLGEQCEAVVRF PRLFQKYPPFILINSAFLKLADVFRVGN NFLRLCVLKVTTQQSEKHLEKI
12021	25922	A	12131	231	330	MDTDEIYLGRAPWLTPVIPALWEAKASG SPEVR
12022	25923	A	12132	95	2	KGKCFPPFFFFFETESRSVAQAGVWRDL SSL
12023	25924	A	12133	129	1	DLALLPRLWCSAMIMAHCNSELMSSSDP PISASQIPGTIGMCH
12024	25925	A	12134	196	361	TIMEYYAAMKKKSESPLLFHQGKKLNQD GGWAWWPTVPVPALWKARTGGSLEPRS
12025	25926	A	12135	120	1	PPPPGLFFFFFFFETESYSVAQAGVQWCN LQSLHPPPPPEFK
12026	25927	A	12136	235	3	KKGIRIERDLRLKQLSVCQRFQAKFPFF PSGVGEKQNFFFKKKKKKKGRAQWLTPV IPALWEAEAGGSFEVRSRPA
12027	25928	A	12137	185	1	IWCPFFFCPGPQICSFRCFFFPFFFPFF LEAETRSFAQAGVQWCDLQSLQSSWVTE LAAAS
12028	25929	A	12138	158	1	LRRGGVFSIFFCGGTMVLSPADKTNVKA AWGKVGAHAGEYGAELERMFLSF
12029	25930	A	12139	76	3	KVLARAIRQEKIKDIQIGKEEVK
12030	25931	A	12140	157	2	FFSSPRLLKRRPGNFLGARENFFFFFFFS ETESPSIAQAGEQWRDLQSLQAP
12031	25932	A	12141	234	388	LSQLMSANLFFVLLFEAEFHSVNRLECS GMIWAHCNLHLPGSSESPASTSQ
12032	25933	A	12142	112	453	LGRRQAASMRREGISIHVGQAGVHIGNAC WELYCLEHGIQPDGHMPDSTIGGGDDSD FNTFFNETGAGKHVPRAAFVDLEPTAID EVCTGTYRQLFHPQLITGKEDAANNYA RG
12033	25934	A	12143	44	443	AKLGTRKLPKAKMGKEITLINIVVIGH VDWGKTTTTGHLIYKCGIDKRTIEKLE KEAAEMGKGSFKYAWVLDKLKADREGER TIDISLWKLDTSKNYVTIIDAPGHRDFI KNMITGTSHADCAVLIDAAGV
12034	25935	A	12144	3	386	REAATMRECICIHVGAGVQNGNACWEL YCLEHGIQPDGHMPDSTIGGGDDSD FFSETGAGKHVPRAAFVDLEPTGIDEVR TGTYRQLLHPVQLITGKEDAANNYARGH YTIGKEIIDLVLDRI
12035	25936	A	12145	3	386	AGATYIDRLRVALFEATFTTLWVRPELS SGEATMRECMSIHVGQAGVQNGNACWE LYCLEHGVQPDGHMPDSTIGGGDDALN TFFSETGAGKHVPRTTEVDLEPTTEIGEE GTGTYRQLFHPQEHMM
12036	25937	A	12146	3	385	GRATYIDRLRVALLEATTSTLRRLRELG SREATTMREGICIHVGQAGVQNGNACWE LYCLEHGIQPDGQMPDSTIGGGDDFFN TFFIETGAGKHVPRAAFVDLEPTDIGEI RTGTYRQLLHPQLI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12037	25938	A	12147	11	381	HTPEGRTRVPVLIAGVVVCQEALRDWGR VTASSTGAMAFRLSMWGVLTALGRSGAK LCTGCGSRLRSPFSFVYLPRWVSSVLAR CPKKPVSSYLRFSSKEQLPIFKAQNPDAK TTELIRRIAQR
12038	25939	A	12148	321	509	YSMDQYFIFPYCQIMHLCFFLKTRVSL FPWLECSGATSACNFCLLSSSNPASA SRVTGIT
12039	25940	A	12149	51	400	AATMRECISIHVGQAGVHIGNACWEL LEHGIQPDGQMPDCKTIGGGDDSFNTFF NETGAGKHVPRAVFVDLEPTVIDEVRTG TYRQLFHPDQLITGKEDAANNYARGHYT IGKE
12040	25941	A	12150	25	399	EATTSTLGLRHQLGSRESTAMRECISIH VGQAGVHIGNACWELYLEHGLHPDGQM PGDQTIGGGDDSFDTFFSETGAGKHVPR AVLVDLEPTVIDEVRTGTYYRRLFHPEQL ITGPEDAANNYAR
12041	25942	A	12151	1	402	TKEEELCLACRQRADGGWRSQMNAGSD PVGIVSAARTIIGSFNGALTAVPVQDLG STVIKKVLKRATVAPEDVSEVIFGHVLA AGCGQNPVRQASGGAGIPYSVPAWSCHM ICGSGLKAVCLAVQSIGIGDST
12042	25943	A	12152	3	400	TDRLRVALKKTTSSTFCFPHHLSRETA TMRECISIHVGQAGDHIGYACWELCYCLE HSLQPEGQMPGDKTIGGGDDYFNTFFSE TGAVKHVPRAVFVDLEPTVIDEVSITGY RQLFRPERLITSKEDAVNIY
12043	25944	A	12153	2	398	GRCALDRNTFIFARFGCYLIASGHPEK LMDMDMSPLRPQNYLFGCKLKAENDYHF IVANDENEHQISLTTASLRAGANDDMNI VEAEAMNYEGTPIKETLATLKMVSQATD SLGGSEITPPSVLRRLKCGSR
12044	25945	A	12154	203	405	FTCPSRICVISRRISPCCAPDLNPLMS ANAMLDVFVTFVEDPGGWDSKNLQKKWSH YSELTGIRPKI
12045	25946	A	12155	229	397	TKIAHHKAGFALISKKITKNLKMFLSKF LPIHALWVTGSSGMQPYPLVWGHYDLGK
12046	25947	A	12156	2	399	GGVPHCVWATAWGMRLPLPGPTGLCAQT SSRGQKSVLKQKESCGIWQLYHFLSRKQ EPRWEPCVSGSSSGDGAVADLADELRGY PALCCTLPVHSYRSWAGIRPQIMNGPLH PRPLVALLDGRDCTVEMPIL
12047	25948	A	12157	85	414	ALLPQSEALQCAVTMPHSYPALSAEQKK EVSDIALRIEAPGKSI LAADESVGSMK RLSQIGVENTEENRLLYRQVLFSAADDRE KKCIGGVIFFHETLYQKDDHGVFPVR
12048	25949	A	12158	85	407	GLLPHSEPLQRAVTMPHSDPALYAEHKK DVSDIALRIGSPGKGI LAAYESMGSMAN PLNQMGVENTKQNRRLYRQDLFRAEDRE KKS LAGVIFFHDTLYHKDDNGVP
12049	25950	A	12159	85	406	VLLPHSEALEGAVTMPHSYPALSGEHNK ELSDIALRIVAPGKGI LAADESVGSMK RLSQIGVENTEENRPLYRQDLFSAADDRE KKSIGGDLFFHDTLYQKDDNGGP
12050	25951	A	12160	275	146	EKTFIISFFFFFETESHVAQTGVQWHD LGSLQAPPPWFRRIA
12051	25952	A	12161	212	2	KRSRPFFFFKEMGSCYIAQVGMQWLFV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GTITACYDPBLLGSKDPPTSASQVTGNT GTHHTQLIFVFLV
12052	25953	A	12162	253	2	GRVDSECCLANGNAEKSIFCCLLVLYFY LSSRQSHSVQAQGVQWHDLGSLQPPPPG FSLLSRVAGTTGARHHDWLI FVFLGET
12053	25954	A	12163	228	1	LLGLWFEQLGRFTKIAKTGERSQTQSG HSMDMRVPAQLLGLLLLWFPGRCDIQM TQSPPAVSASVGDRVIITCR
12054	25955	A	12164	122	1	RLLFFETESRSVARLECSGATSAHCSLR LPGSGSSPASAS
12055	25956	A	12165	239	350	GQARWLTPVIPALWEAKASKSLEVRSLR LAWAGHGGG
12056	25957	A	12166	235	359	TDKAISKRDLSVLREIIFEMESRSVAR MECSGVISARCNL
12057	25958	A	12167	209	396	QFSGIPFDQYKCGFKNYIYIYIYIYI YIYIYRKYTRAYTKRYMCVFSRATHNIV YLCAYI
12058	25959	A	12168	327	130	GGVGFLLGGPGEKPPRPSPFFFFFFEKES RSVPQARVQWPDFGSLPAPFPFGTFFLR ESFLFSSLM
12059	25960	A	12169	317	422	RGEKPLFFFLQKKKKKKKKKKKNIKKG GRRYKPS
12060	25961	A	12170	260	375	EKVTCSWTQWLTPVIPALWEAKAGRSLE FRSLRSAAI
12061	25962	A	12171	304	3	KFFFFFFKGFFFLGGVGPIFPKKRFFS KIPPGVFFFPPLKKKIFFFFPVILGPP RVFFKGAPLEFFFFFFFSETEFRSC CPGRLECSVAVAHCK
12062	25963	A	12172	105	3	LIFLRQSSALLPRLECNAGTSAHCNLC TGSSD
12063	25964	A	12173	146	17	RIFFFFFFLGQSLAVAQAGVQQRDLGSLK APPPGVHAILLPQEY
12064	25965	A	12174	234	2	LFPRKPKPSVLSLSLSLFLRLRLKLS FMRHNNIEVRPINNPAMTSKCSERKSL VSFTLNLKPGMIRLSEEGMLK
12065	25966	A	12175	292	380	VRGLGRVAHTCNPSTLGGQSGWITGGQE F
12066	25967	A	12176	109	1	GRIKKVIKQAQWLMPVIPALWEAKVGG SPKVRSSR
12067	25968	A	12177	170	291	LINFYFYFLRQSHSVTQTGVQWCNLGSL QPPPAARRRRRG
12068	25969	A	12178	260	380	LTYIALFI FLRRSLTLPRLECSGMISP HCNLCLLGSSDS
12069	25970	A	12179	54	166	PKRGFHRVTQEGLNLLTLGSPRLGLPKG WDHRQDPLP
12070	25971	A	12180	273	359	APAGHGGSCLOSQHFGRLRQADHLGSGV R
12071	25972	A	12181	27	225	IGQAQWLTPVILAFWEAKAGGSLEVRSS RPAWPIYFLVLLASYLRRFCLIQGHSDL LYTSSTRGS
12072	25973	A	12182	1	155	VHKIFIAKYSGFQTVFRGRAWLTPVI PALWEAKANRSPEVRSSRSRGRG
12073	25974	A	12183	91	2	FNLFFFFFFFETGSRVARLECNAGTSA C
12074	25975	A	12184	122	2	GQAQWLTPVIPPPWEAKVGKSPPEVRSSR RTRGRTRGRTRG
12075	25976	A	12185	389	20	TDRGRRARRACFCGKVFDELSFALKLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REMGRPDRAMLAGMSSTEYADWHRFYS THYFHDVLDMHFSGLTYSVLSTFFSDP DMHPLDFSLNRRREADDEPEDDVLMOQA AGLAGGVLFLLI
12076	25977	A	12186	180	393	LNPSSGGCGEPRSRHCTLAWVTERESVS KNKIKIKINKQIEEGFLFPFGQGF IWC YFPAKEFI IALSKT
12077	25978	A	12187	37	443	PDFPIPFPPRKVQHLARPSPKTARPAWT IRRILPPPPKKRHPGGLARGKFGPRELA KAGLAKECPAGGPTPAVRPATPTRGGGG RVAGFQTPMGIPMGKARLGLLTFLGFAS GWIGAYRPRETLCGGELVDLTQF
12078	25979	A	12188	3	411	AFPENAAATGSTFQDPVPASKGRAEVDNM RLSVAAPISHGRVFRMRGLGPESRIHLL RNLLTGLVRHERIEAPWARVDEMGRYAE KLIYYGKLGDTNQRAMRMADFWLTEKDL IPKLIVQLAPRYKDTGGPTRMLQ
12079	25980	A	12189	2	414	QEFGRTRKRTFISLLFFSSVYSRGVFR RDAHKSEVAHRFKDLAETLRLALTLIAF AHYLHQCPFADHVKLGNATEFAKTCVA DESAENCDKSLHTLFGDKLCTDAPLRET YGEADCCAKQEPERNECLLQHKDD
12080	25981	A	12191	3	514	PRLLMEAGPHPRPGHCCPGGRLDMNHG FVHHIRRNQIARDDYDKKVKQAAKEKVR RRHTPAPTRPRKPDQLQVYLPRHRDVSAH PRNPDIYESGESSSSGGSELEPSGHQLF CLEYEADSGEVTSVIVYQGGDPGVSEK VSAHTPLDPPMREALKRIQEEIAKRQS QH
12081	25982	A	12192	182	3	RGLFFIPIPPPIKTKIWGPFWKVVFMGFG PPLFFFFFEMESRSVAQAGVQWHDLSLQ ALP
12082	25983	A	12193	53	400	PETPSWLGPVRRFYFIIKSVWKWKKKK KKKKKKKKKKKKGGGPKKTLGGDKFYW GVKKKIIFFLGGSKKHPWGFFKELFFG GKCGAPPKDISCLWGKKNFLGAIGEK TCCC
12083	25984	A	12194	182	3	KGIFIQIAPPKKKKNWGPLWKVVFKGFG HPIFFFFFEMESRSVAQAGVQWHDLSLQ ALP
12084	25985	A	12195	200	378	KSSKSQWLGYLFIGLLTYLFKFFLETR SCFVTQAGILAHCNLKLGSDDPPTSAS QAA
12085	25986	A	12196	341	54	SLSFHGGLSVLCIFSTYKKLSQEQWLTP VISVLWEVKVSRSPQVRSRLRPGDPPASA SQSAGITGVSHHARPHLSLNPRLMIKL SEEGMLKRMTG
12086	25987	A	12197	1	462	GGPPRPFRMKAAVLTAVLFLTGSQARH FWHQDEPPQSPWDRVMDLATAYVDGLKD SGRDYASQFEGYALGKQLNMLLDNWD VTYTFSKLREQLPVTQEFWDNLDKETE GLTHEMSKDLEDVNAKVQTYLYDFQKTW QKELTFTAESPEVP
12087	25988	A	12198	80	1	SNKVFFLETESCSVAQAGVQWCDLGS
12088	25989	A	12199	221	3	TMGIMLDKKEIQAI FSKFKMGHAVAET TCNINNTSGPGTANKVTVQWWFKKFCCKG DESLEDEHHGRRLEV
12089	25990	A	12200	239	336	FGALPITTCFKGKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKKKKK
12090	25991	A	12201	279	366	KKKKKKKKKKKKKKKKKKKKKKKGFK
12091	25992	A	12202	153	40	GFLFLIFFFFTETKSRSTIIQAGVQWCHLGCTLAWATETD
12092	25993	A	12203	317	406	LGKLCNGAVSGHCNLRLPGSSDFSGSAS
12093	25994	A	12204	2	925	RSQPDHELTLDGKGGCTSRMVPASAASE DRRLKLP I IVEDEGGPTRSRACSSPARGS RPPPSAIGCSPVAQASDASAAGPARRTAL QSLSSWLGYQIDRHSVPVYVFKSPLFSV IMAPKHKSSDAGNLRPKRSRKVLPLSE KVKVLDLIRKDKKSYAEVAKIYGKNESS IREIVKKEKEIRASFAVSPTAKVTATV RDKCLVKMEQALHLWVEEMNRKRVPIDS NMLRQKALSLYQDFSKGCSETDTKPFTA SKGWLHRFRHRFHHYKKKKKGIMAQVA VSTLPVEEESSETRMVVTFVLVSALESM
12094	25995	A	12205	272	1	KMARAGLLVIEGKVVWRTVYYRFATREER EGKMSTNLNMKLDITIGFDNKKDILLISVG DLVDRGAENVECLELITFPWFRAVRGNH ERQPGQ
12095	25996	A	12206	166	478	ISASGLLPTSPLTGTSTKLQDPNEHLNLL MLNRSVSLLLPRLECNDTILAHYNLRLP SSNSPDSAFQVAGITESFTCEINALKDS SQVALWSFRCEMDHSSICNR
12096	25997	A	12207	102	497	PLLALLFGSQKTFCLQLSLKPTRSSLL SPGSAGNPENEAPCPQLNPEATSLKKKK KKKKKKKKKKKKKKKKKKKKKARG
12097	25998	A	12208	131	2	FGFLGGDKAKGKGGPPPPPPFFETESPS VAKAGVQWC DLGSLH
12098	25999	A	12209	221	499	QTRHKLTNSRSRGRTGLQILIKEQHSSGR WCGTGDILWQSL EDTICYVPKSLDLDFL LFIIYFETESHFVTRLECSGAISAHCNLR LLGSSDSPA
12099	26000	A	12210	297	398	HNFFFFLKTESCSISQAGGHWYDLSSPQ PPPPG
12100	26001	A	12211	341	452	NWSPGLKQSSRLSLPKCWDIRREPPCLA GLLAYLFRR
12101	26002	A	12213	214	468	FFFFFFWGKGVFFFFPPLEGRGGNSVYW TPPPRGKKNFPPLGLGKMGNNPPPPPPR FFFFFFFKKGVFFLPGPGVKTPSLRETP P
12102	26003	A	12214	223	477	CPTETQLQLIFAREKHKPSPVLLDLDL Y GFFFEMESHVSVPLECSGPISAQSNLYL LGSHNSPA
12103	26004	A	12215	263	55	TPKRYGKMQTATYLPKSKIYIIISDLRK QDYIVYKQSKKPEGWAQWLTVPVIPALWE AKAGRSKPKVRSSR
12104	26005	A	12216	328	471	GVLIHAQVLHAHTHTHTCTHTQVHAHS
12105	26006	A	12217	434	1	WDHSASPTSVGTPLRADGPHPRLTAPG HVGSSAMLSAPAAGRRLSLGRWC DRD KLSQRGPQPKWILWWGNLEGGGFLHRHI HKPLPTIPIPSTVRGEEVLQQLLHSASF ILFIFI FLDRVSLCHPGWSAVERSFTT TSTS
12106	26007	A	12218	304	43	EKPIGVAPSRVKKRAGGGEKTECCLLKG PLQGFQGV LKGPLKLNGLPFFFFFLRRS LALERLECNGTILAYCNLC LLGSSDSPA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SEI
12107	26008	A	12219	171	365	ALVQPRAGREAVTVPACCSCSDVFLYET NKVARIQSINYGTIKFFHVIVFSYSKE HLKRKLEK
12108	26009	A	12220	171	452	ARYKFLHPKFAFGLYPSSSIQGARHQL WILIKCSFYLLFLRQCCLLPQLECSNM ITAPLQPLPLKQSSHSLPSSWDYRH EFP
12109	26010	A	12221	323	458	FRVQRSLFLFIYFFETESHPPVQAGVQW HDFGSLHRISP
12110	26011	A	12222	189	56	DRVSLVQPTLECSGTISVYCSLNLGSS DPPTSASPVAATTGGI
12111	26012	A	12223	246	494	FLCSSYAYDDHFLRPFPIHLILDITAF SQDTIISNLLFQDACSVPKAANLGOAQ WLAPVIPVLWEAEVGRLLVRSRPAW
12112	26013	A	12224	55	353	RIQGCSCWVKLCPKVEKVVQRTDAEQES QTKAEIQDMKQELSAVNMDKFARSARL ERKINKMMNKLKTHVKVQTAQSGMLKWV ISVAFYKLPGTVIRL
12113	26014	A	12225	199	23	LKLSIIYYVPGTILKYFTGWARWLLPVI PALWEAEVGGSPVRSRSPANSTSWIER HQ
12114	26015	A	12226	369	14	DCVRVGLSYPQTVCPSCSVRKAPFSSR PHRGVLESGQPRCKSRVDIFFSMERER DRERERERERERERGQKRTTRVWGGERE KLGYSYHAWGWRGGRGLWGGMCGIPPPC TSDVHQ
12115	26016	A	12227	206	2	QNGHMNGGPPCRVLSLFLFTRSFLLFLA SLSMLECSGAILAHCNLRIPGSSNSPAS ASQVAGITGACH
12116	26017	A	12228	231	501	RSWEGQALHGSDPLASCTRIQSNYMALQ RINQLEEDKLYRMGQHYEBEKRALSHEI VALNSHLLLEAKVTIDKLSEDNVSAHTW PMEDCR
12117	26018	A	12229	86	455	DLPTFPVPPHFGSGPLLGQSELPSNCQ TGGRSHLSVSVLCPTLATPLGLDFPTC GTSQLPLGLQLAHRSELAGLSPLGLST NCTSQRLPDRPHRHSAPHTHTHTQHT HTHTHTPATVT
12118	26019	A	12231	211	96	KSHFKAGGGPPRYSPFPGGGGGVFRV GGFPPPGLTQ
12119	26020	A	12232	228	3	KRWFIKGLSKGLGPPPKLKLGLGFFFF FFFEQSFVLVAQAGVQLECSGTILVHFN LYLPGSSNYFASASHPRV
12120	26021	A	12234	137	3	VPLPGTLKNHSMVPCFLFVCLFVCYETE SHSVAQAECGSAISAH
12121	26022	A	12235	139	1	FKLCFGQAWFKPIIPALWETDASRSLE VRSSRPADAWADAWADAW
12122	26023	A	12236	80	1	VLLIFIFLEEMGFHHVGQDGLDLLTL
12123	26024	A	12237	187	494	TERNSFNINKKDIHTKTPFVGYQHRPK VDKTTKMGQRNQRKAENSKNQSTSSPPK DRSSLPATEQSWTENDFDELTEVGFRRS AITNFSELKEHVLTRTE
12124	26025	A	12238	252	503	CQGVGADDLQSQAEIQELCAESIDRFD ILFFFFLGLGPPHKNPPPTPQKWKPGK APPLALWDIPRGAKGPGRQPGRAIHTC
12125	26026	A	12239	2	471	RIALCPAVRIRHEERERERERERETP GHTQLSPGARRTPLERERAFNDCPSLN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YPGNLCPGDLIEVFRSVYQHICALYLGDG YFINITPVYGI PAFFTS AKSVFFSRALE KTHLLKD VVGSDTYRINYICYETLPSLS VEEIIITRSEFVIGQEA
12126	26027	A	12240	14	149	FMTACRIRHEMGRGLRLGLWPLHIVLWT RIASTIPPHVQKSALPH
12127	26028	A	12241	588	671	RSRPSFQEQAFESSQKYKEGKYIIELNH
12128	26029	A	12242	384	464	RGGQVWVWKPVVPALWEAKAGRSLEAG
12129	26030	A	12243	325	459	TYLFIYLFYFETESCSVAQAGVQWRDL VSLQPLPNSPALPTN
12130	26031	A	12244	323	457	SLQRECGPADTFFEMDSCSVAQAGVRWC DLGSLQNSP
12131	26032	A	12245	241	466	GALFFFFFFFFFFFFFFFFFLSNKAVY F
12132	26033	A	12246	385	37	QARRRCLQTSRMEALGRWSYKVTIEFPL QILFFPPILKYKVI FGKITPNPHFLEE YEEGQRLGKSTVSWVFNEDTRLINIWNR HITVNPR TNSQNRMLMAHESKYSQVPF PLQA
12133	26034	A	12247	318	456	LILKYFMYVCMYVHMYVCMYIKSCSVAQ DGVQWYDLGSLQPPPPGL
12134	26035	A	12248	362	473	SPCQNNMNSAKTEARTNIKFMALMWKN GAIIDALQK
12135	26036	A	12249	310	463	FSIKTRKNALGKLQSLRCHQFYLYVCV CVCVCVCVCVCTRTYAILTCIAV
12136	26037	A	12250	169	54	EAKSGQARWLTLPALWKAAGGCPEV RSSRLAWPIW
12137	26038	A	12251	49	449	GIPATSTSCVQVILLPQPPLLLGLQDSF LPQEIIIKVEGEDTGS LTIPSGE VNFK IVTVDF TREEQGT CNPAQRTLD RDVILE NHRDLVSWDLATAVGKKDSTSKQRIFDE EPANGVKIERFTRDDPWSSC
12138	26039	A	12252	130	428	RWGLAMLPRVLVNSWSQVILFPQPQVGA TFGGFPNPPGHWKLLGGISSGEEAGVEE ABEGQALGLGQFPSPQLLLQTSWCL RTTRTCRWSLLWKAH
12139	26040	A	12253	204	54	PGMHKTQKSDLGQVQWLTPVILGLWETE AGDSPESRSPAPAWAKHKIVR
12140	26041	A	12254	375	470	SLCLFFSFFFQTEPRCVAQAGVQWRHLS SLQP
12141	26042	A	12255	432	512	GQVRWLTPVIPALWEAEGGRSPPEARSS
12142	26043	A	12256	232	1	KGALSKKTQSFWGQKFFPRPGVFGVVF FWGGGFCFFVFGGFFFFFFFFFETESCSV AQAGVQWCSLGLSLQLPPLPRFK
12143	26044	A	12257	22	123	RFVCSTIKVLRDLSSDRSNPGRFLSTSN SSSTRP
12144	26045	A	12258	71	362	QTERNSISINKDVHTETPSKGHQHQRP KVDKSTKMRKKQRKKAENSKNQNASPP KDHNSLPAREQNWTENEDELTEIDFRR WVITNSSELKEHV
12145	26046	A	12259	375	3	SPNIEAPPKAFFFFNQRHFVFCFFSCRA ENTHEIVVVKVYPFSNQSKALFFSFFV QRDRSSPDSYLMPLQLQMWDTAGQERFR SIAQSYYSANALILAYGITCEESFRCL PEWLRQIEQYA
12146	26047	A	12260	98	1	KYQIDLGGRGSSNSPASASRVAGITGTH HHTQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12147	26048	A	12261	125	3	LFLIQKYITGQERWLTTPVIPAPWEAEAGRSPKVRSSSPA
12148	26049	A	12262	228	385	SCLYLQMTIPSSIEKSQGYMKATRGRARWLTPVIPALWEAGAGRSPEVRSSR
12149	26050	A	12263	227	369	MLKHKSNNKLDLQGMQGLTPVPNPVLWEAKVGGSPDEVKNSRPAWPTW
12150	26051	A	12264	102	487	QQNRFFGTERGRGTGRGVSSFPQLSPGSLLEASSPSPSVGRLGSAASQSRSGGQERPKAQLRRPPRPSSSPRLRGRENCAHHARTPGGILDRBPPTLGTNLLKGGRPAAWMAGNPPEAHKTANGPGEQA
12151	26052	A	12265	391	476	PRSYRVECSGISAHCNLGLLGSSNPSS
12152	26053	A	12266	378	476	MSSRLGSLVGLGRAWLTPVIPALWEAKEGG
12153	26054	A	12267	166	58	NFFFFFFFFETDSCSVAQAGVQWHDLSHCNLCLPASSN
12154	26055	A	12268	209	49	TPPNFYIKISRSQQAWLTPVIPALWEAEAGRSPEVRSSRPASPTRNSISNS
12155	26056	A	12269	127	1	SSSFFFLKTFGLFFFLCFFESERSVAQAGVQWCHLGLSLQA
12156	26057	A	12270	154	27	IQTPGKKEFFFFFFFFETKSLVAQAGARLCPKKKEKENSNFVL
12157	26058	A	12271	180	22	VLKIHNIQRAQWVTSVIPELWEVKAGGSQALRSSRAARTRWDACNFVEKTQVY
12158	26059	A	12272	207	422	GDSSTRGADEKPKKEGVKTDNNNLINLKVMGQDCSMQFKIKSHIPAGYGGSHRESQHFVMPRWADHLRSGV
12159	26060	A	12273	59	479	NSLGGGGVYGSRRFTFPGCRALSPWRVRVQRRRCCEMSTMFADTLIVFISVCTALLAEGITWVLVYRTDKYKRLKAEVEKQSKKLEKKKETITESAGROQKKKIERQEEKLKNNNRDLMSVVRMKSMAIGCF TALMG
12160	26061	A	12274	354	439	VKTGECSTAKTWNQPKCPTTIDWIKMW
12161	26062	A	12275	366	499	TRAQYFVVVVGIGSQCVTLECSGMIMAHCSLDLLGSSDPPTSAS
12162	26063	A	12276	136	37	KFPGQVHWLKPVIPALWEVKAGGSPEVRSSRPA
12163	26064	A	12277	419	48	DGKLVNSFLTSSSGCFLIFLLIVRPPYFLRYNNSEIRPINNPTMTCKCSSKRKSRICLTFNQKLEIIKLSEEGMSKIKTGQNLGILCHVSQVVDQHKFVKATKSATAKINLSISKYIMSGA
12164	26065	A	12278	190	1	RKGVFSPQMGPGLGKSKSPFLAKLNFPFKKTFFFFFFFFETGSCFVAQAGMQWLDPSPPDAWADAW
12165	26066	A	12279	276	389	WFNLSFFCFCLFFETESCSVARLECSGAISAHCNLT
12166	26067	A	12280	425	1	PPHPPPGKPPPPPRPELFFPKTKNKKERVLFFSPPPKKNFFSLTTPRFFSPPQKKKKKLNPQQKGPVPIKPPPLFFFFFFFFFFFGLTVRVIMTCWLIVDIGLLI
12167	26068	A	12281	253	90	IWPPQGSFKTAAPFFFFFVFLVEMGFCHVVQAGVKLLTSSSPASASQAEKLF
12168	26069	A	12282	61	387	PKSSSSAPFQISSWFSLPASTSASTMSIRVTQQPYKVFNSGPWAFSSSSYMSRPSAHISLIVSRVSSSSTSFQGGGLGAGMGLP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LHSSLANRRLSQKKKKRGGRSKEP
12169	26070	A	12283	186	305	LHSTVQVRREEHKSLSHTQVHTHTHTHT HPHLVIMSSHS
12170	26071	A	12284	2	190	PRVRFDRVNNRSLNPLISRTMTRIEPIPE NPKFSVKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKGGGA
12171	26072	A	12285	17	197	SLGVGGGQGGGGVHFHPCKPFIVLSPVS LSKHCSYLPKKKKKKKKKKKKKKKKKK KKKKKKKKKKK
12172	26073	A	12286	158	405	GVASAEQRKYFLEMEYFPGGEAISTIVE MTEDLHYSINLDDKAPTGFERYVSHFE RTCTDDKMLSICYTCYREIFCERNKL
12173	26074	A	12287	364	142	GCAFFLGGPLKERRKRRVPPPLFFNFNF FETESCSVTQAGVQWCNLSLQPLLDW WQPGTVAHACHPGTLGG
12174	26075	A	12288	171	380	VFEAGHAWLQENLTSPDFWGFSPFPTDT GMLEKKKKKKKKKKKKKKKKKKKKDR
12175	26076	A	12289	194	2	GERGFQWQFWTKGFFPKGFVKFYPPAG GWFFFPKRGFPFSPFLFFFDRLVWCHP GWISVARS
12176	26077	A	12290	179	416	LIFLFTFACAVCFQLARFHKIHIETAL RCLIIILSCPFTHPLYKMYREGQARWLT PIPALWEAEVGGSPVEVRLRPAC
12177	26078	A	12291	3	408	LAYGFHRTTYDTSPALMMVLLVDELIT GNKNGSGEAPYLPEDFRDGEDDAVTL EKQEDLTTLVTLPVTLGEHQRETQLE AKLLKKRLELGSLLDLVEDLELI IQLKK KKKKKKSPWGAFFKGPLGAPI
12178	26079	A	12292	119	278	PKSIEAGVKSVDHPLPNKAKTHLSCKK LKKKKKKKKKKKKKKKKKKKKKKKKKK KKKK
12179	26080	A	12293	119	3	MLFTGFHTKVMSLNSTGWAWWFTPVIP ALWEAEVGS
12180	26081	A	12294	205	1	ILHFYSTETKQPKGLFLALFYSDCEQEK RKGGKLLKIFKKAQGOARWLTVPVPAFW EAKVGRSPEVGS
12181	26082	A	12295	215	1	AFKIKLTMHIFSSPLCLPQDEFHPFTEA LLPHVRAIATWFNLOARKRKYFKKHEK RMSKEFHGARLEGNO
12182	26083	A	12296	185	411	DVPLMFHWLHLHSDFRISTEIGVETVG KRVLHIRILLLLLLLFFEMESCSVTHAG VQWCDLGSLOAPPPGFTPF
12183	26084	A	12297	281	388	RILFFFFFFETKFCVSPQAGVQGRDLNSL QPPPPGFM
12184	26085	A	12298	178	3	TLLSVTQVPILPGSASSPLLFSSRKDIKI PTSVFFSFQTEPRSVTQAGVSWCDLGS LQP
12185	26086	A	12299	199	450	TLIRHMICNYFLLSHRSPFSSVDYFLCY REIYSLIKTLNKLIGGFFLNI IKVMYD KPAASIRSEKQKAFPLRSCTRIRCP L
12186	26087	A	12300	3	407	EFKDHSTAMDTEPNPGTSSVSTTTSTT TTTITSSSRMQQPQISVYSGSDRHAVQ VIQQALHRPPSSAAQLQQMYAAQQQHL MLHTAALQQQHLSSSLQSLAAVQASLS SGRPSTSPGTSVTQSSMVQTSI
12187	26088	A	12301	227	3	KRGTEGQTLFFPAPRARKSFPPPKMPKK VEKEFPKGFFFFFFFFFETESAPSPRLCS GAISAHCSLNPHASAHAS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12188	26089	A	12302	292	380	KCYRWARWLMFVIPALWEAKAGGSLEPRN
12189	26090	A	12303	13	186	VDERHIRLSEMAWVALYLLSLLWATAGTSTQTQSSCCEYDVFPRRSGKQLPWGRGCDL
12190	26091	A	12304	253	409	ITAVIAAAAAVVGVTIIMTNFRSLPRLECNGAISAHNRLLLLLGSSDSPASAS
12191	26092	A	12305	153	64	GRAQWLMPITIPALWEAKAGGPLDVRSSRPA
12192	26093	A	12306	265	420	GTLMSRNTKLQLCRMNKSRITLQGPWWLTPIPTLWEAKAGGSLEARCSRPAW
12193	26094	A	12307	295	1	RPCLKNKKTSPHWKKKFANPLFGKAPVFPDCKKPFKPHYRESRPLKKNKNGPKGFFFFFETESCSVTQAEVQWRDLGSLQAPP
12194	26095	A	12308	247	421	SWCCLKKKKKKKKKKKKKKKKKKKKKKPGGGALKKKKIFS
12195	26096	A	12309	168	3	GQALLLLCLTVAFSKTTVVCHAPILGWAWWLTPVIPALWEAEVGRSPEVRRSRP
12196	26097	A	12310	117	3	VAYNIAVFRGGVSLLLPRLECSGVISAHCNLRLLPCSS
12197	26098	A	12311	256	101	EEPTPFFFFETGSCSITQAGARRDHSPQPSPTPGLSNTAPASRACESGR
12198	26099	A	12312	146	3	FVALCIQLFPLVNVICFHKKHKTGRARWLMPVIPALWEAKAGGSPEV
12199	26100	A	12313	207	3	VRVRTTGVMIALRGLCFVSVEESMTKDELIALRLSLGELNDRDVSITGTKEELALRV
12200	26101	A	12314	282	2	NCLAELKVKFMVSAISLQPGISILFLSF
12201	26102	A	12315	298	84	FFEKESCSVPQARVQWPNFSSLSQPPPGFKLFFCLSPGGGGCSEPKSCRCIPGWQQNETPSQKKK
12202	26103	A	12316	124	1	KTQPQPPVFALSKNFGPPKTAPIFFFFFFFETKYSVAQAGVQWRDLGSLHSSLGHR
12203	26104	A	12317	132	398	ARLHLKKRKRKSINL
12204	26105	A	12318	262	392	SKGHFFFFFFFSETESCSVAQAGVQWHNLGSLQVPPPRFTPF
12205	26106	A	12319	168	3	VVTNAVFSIVTFSPSVCHSEVALAAYKWLV
12206	26107	A	12320	48	385	CYLLRETYQKLNQEIKPPTLSVPKKKKKKKKKKKKKKKKKKKKKK
12207	26108	A	12321	218	83	PHYCQNQPQARRSGSHQHFQKQRRDHL
12208	26109	A	12322	197	1	SLGVRDQPGQYSETP
12209	26110	A	12323	128	36	EAPKAISNCTTALQPRLOGKNLSQNKKEG
12210	26111	A	12324	140	3	QVQCLTPVIPALWEAKVGGSPSEVRSS
12211	26112	A	12325	273	369	DLGLSGHSTLASSFISLLLLSYKKCLSP
						STMIMRLPLPCGSPKIPFPLPKKKKKKKKKKKKKKKKKKKKKKTGG
						NLSPIFPEGNFFFFFFFEMESRSVAQATV
						QWRDLGSLQAPPPRRKF
						KETWFPFPPKKEQGLFSFFKKRIFFFFSK
						KIPSPPPPPPPFFETESCSVAQAGVQWH
						DLGSLQAPP
						KGLFFFFFEMGVSLLPRLCSGTTSAHCN
						LP
						ILNSNLKPIKKNITFFETESRSIAQAGV
						QWHDPSKQPPPLGFKR
						RKEWFLKKKKKKKKKKKKKKKKKKKKTKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKK
12212	26113	A	12326	140	415	RTGLLGPGRLLQGPYPYGSREYKSGLLDL NASLLDPEVWAPSLSGPETKPPAHSPSD PGVHSSCSASQGSQGPPLTPSSRIHEP KPPGPFCK
12213	26114	A	12327	2	506	FVPLSETEAPGCSGSRPPELEPERSLGR FRGRFEDKDEQLEEEEEEEEEEEEEED MSHFSLRLEGGQDSEDEERLINLSEL TPYILCSICKGYLIDATTITECLHTFCK SCIVRHFYYSNRCPKCNIVVHQTPQLYN IRLDRQLQDIVYKLVINLEEREKKQMHD
12214	26115	A	12328	1	419	FRVPSCARCQYLPLLRGASQLGYSVGRD PVEEAVCFPSDLKLCAGRTTTLFKAQRQ GHLSLQRFLPFFVWLCAPRSGVYRGRQ ASLSCGGLHPVGASWPRCLPTQASAMAG TPPPASLPCCSLISDCCASNERGSMGV
12215	26116	A	12329	259	414	NMENSLRCVWVVKLAFVLFASLLSAHL QVTGFQIKAFALRFLSEPSDAVT
12216	26117	A	12330	302	404	SCYRVSVISQARWLTVPVLPALWEAEVGR IPEVGS
12217	26118	A	12331	94	375	SRDMSPGLLTTRKEALMAFRDVAFAFTQ KEWKLLSSAQRTLYREVMLENYSHLVSL GIAFSKPKLIEQLEQGDEPWRENEHLL DLCPGWSAMA
12218	26119	A	12332	7	246	NPIVDPSPCGGIRVRTPAGRGPPALRVR PETWEEAGEKMPSESLCLAAQARLDSKW LKTDIQNCFTIRKISLLPLFCHHL
12219	26120	A	12333	150	1	YIYFFHLVRGLPGSGYDEYFVVVVVNT SPSVTQAGVQWCHVVSQVHKPP
12220	26121	A	12334	34	426	BPGFLFVFFFLIRGKKTPLFFWGTRKNP KSGKPLFTPPGKSPSEPPKSRGGPLFFQ TRSRLLTPQSWFGGAPKPLGGEPPKFEW AGLGGDPPTPRAPHRADQTLQPIQAPT RIIQNEQWAIKPFQPMPPG
12221	26122	A	12335	185	3	TVITPLHFSLGHRARLWSRVPAPPAENR SMEGGLGRAVCLLTGASRGFGRTLAPLL ASHE
12222	26123	A	12336	60	316	GWGPIPSTDVTVLSPQKPILLQGERAI TQIKYNREGDLLFTVAKDPVSVGWRGSG RGGILLPGRWVDTVPVLPAGNQASHCE K
12223	26124	A	12337	3	167	SFRIQVQGNHTSKHYPKIQYSDQAQWLT SVIPALWEAKTGRSLEVRSLRAFRA
12224	26125	A	12338	238	401	RPLSVMCGRLTSIRVEDSGARCWFYLF YETEFRSVAQAGVRRDLGSLQTPPSG
12225	26126	A	12339	354	433	GWAQWFMPVLPALWEAKAGVSPEVRS
12226	26127	A	12340	238	382	LLIVYNMMLLPDAVAFTCNSSTLGQGR RITRGQEFETSLANMVKPHL
12227	26128	A	12341	101	1	KTQNTNKKTRSVGQTWTFPIIPAYWEA QAGEL
12228	26129	A	12342	276	23	GSCLEGLTNRKDIHTKTPSVRHHQR PKIDKTTMGRNQSRKAENSKNQSSSP SKECSSLAATEQSWMPHDFDELREGEFR
12229	26130	A	12343	122	1	YMGVNERGCGQSIFKSSSLSSQLWWAF IPATQEAEGEW
12230	26131	A	12344	180	360	LHVVFYFVSGDFLPPPPPLDDSSALPS ISGNFPPPPPLDEEAFKVQVRAEVKVML GKS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12231	26132	A	12345	35	411	TMTIVDKASESSDPSAYQNQPGSSEAVS PGDMDAGSASWGAVSSINDVSNHTLSLG PVPGAVVYSSSSVPDKSKPSQKDQALG DGIAPPQKVLFPSEKICLKWQQTHRPGA GLQNLGNTCFANA
12232	26133	A	12346	278	386	ITICYKQTIIGQARWLTTLIPSLWEAKV GGSPEVRS
12233	26134	A	12347	111	2	KSQTGQVQWLTPVIPALWEAEVGGLEL RSSRLAWA
12234	26135	A	12348	215	316	LNKRLMISFIKKKKKKKKKKKKKKKKKK KKKKKKKGGPL
12235	26136	A	12349	265	404	SNISYFLNNNFSKALSNIKYMISQARW LTPVIPALWEAKVGGLEPE
12236	26137	A	12350	372	1	PVFPLPPKKLGEQLPPPALRFLAVSPLP KAAHEQEIKEKVLAVHKNPIDPVYGFPK KGPTNFFLPLFQRVIFLGAQKGVSWSFG FYVKGLSLAPKLGGPPFFFFFETESRSV AQDGVQWCDLGS
12237	26138	A	12351	318	416	OQRAQWLTPVILTLEAKAGGSSEVRSS RPAPP
12238	26139	A	12352	144	1	NGYAIVECVVLFCEVFLRQSLSVAAQAG VQWCNLGSMQPPSTSLVQAI
12239	26140	A	12353	116	1	SGRYSFKMKCGQERWLASVIPALWEAE VGRSPEVRS
12240	26141	A	12354	102	2	ETRYKKQPGCWERWLTPIIPVLWEAEV GSPEV
12241	26142	A	12355	112	294	LISPCPMWPSPHGPTWLSRLISQHS NLKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRGGAFF
12242	26143	A	12356	138	2	SFFLKVFFFFFFFEMESRSVAQAGVQWCN LGSPQAPPGSRHCPVD
12243	26144	A	12357	148	394	PGEPPGEKGGGKGGKPGGRGWGEPPCR GGFKEKFPRGKEKAPPLKENSRENLGW TKIPPLGKKKPPPPQEQEMILGPPQF
12244	26145	A	12358	97	3	EKFSPCFVRARTHTHTHTHTLSLSLF GFH
12245	26146	A	12359	204	2	KHYTPAACFAPCLPDEAPIIAAKPAT TSEQKMAVPPKYANLGKSARNVFNKGYG YGLINLLKTKS
12246	26147	A	12360	156	391	NRGLFKVEESFSPICSVRCSIHPSALVS PTPPTDITTNWALFFETESCSIHQTGMR WRDLNLLQPLPPGFKRFSCLNL
12247	26148	A	12361	179	1	ALKKLLIIDDNSHKTNIKHFSPFRNFTF LFLLETESRSIARLECSANPTHCLRL SGP
12248	26149	A	12362	218	391	TILKDCFTKMICLSQAQWHIPVVPATWE AESRGLLEPTS
12249	26150	A	12363	2	356	TNSHVDNSITQKPEFCIPRCCGYIVCQL QLVERAFIFNFFFFFFLKRFSVLLPRLEG RGAI FRVTQEGSNLLTLGPAPLGLPKGW NYRGDHPGPAYFYFLMGKRLQLIQGGRG LKRNL
12250	26151	A	12364	94	1	KNPPLFFFFFFFESSESCYVAQTAVQWHD LGL
12251	26152	A	12365	237	2	YSSLLFKPAESAKGILRHHVTPKSTSAI SKILFCFLFFVETFLSPGLKCSGAIKV HCSLNLGSSNSPTASQVPGS
12252	26153	A	12366	340	442	GLFVCFVWFLETESCSVTQAGVHWCDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSLQPS
12253	26154	A	12367	208	45	EGGEFFFFFVSFFFFVRAGVLPCCPGWS ETPGSSDPPALASQSAGITGATVNST
12254	26155	A	12368	60	443	CSSCVSSKQSPHLKKQGRMGHLSG GCTEATAGKMRKCLVAWSTCAGARPPS RNRGSQGHSAFQGPRLPTVVRLPPPPP QAKPFCKKWLGGPISIEPKPQHPPGPG KKKWAGKAAPRLVPT
12255	26156	A	12370	341	421	SGWVRWLTPTVPALWEAEAGGSPEVGR
12256	26157	A	12371	280	393	NTIDHYVTQWLTPVIRTLWEAEAGRSPE VRSSRSAPWT
12257	26158	A	12372	268	399	TLCSLSAESIIHSYPFESCKDNYLMTH NEAYKACMRRAFHIP
12258	26159	A	12373	209	468	EAVPDETSHPSPADSFTSSNLACGTHH LRRLKLKYVEEELEYPRKIQCFFHSFF FFESRSLLLPRLECSGISAHCNLCIL GS
12259	26160	A	12374	381	488	TITCLFQKCQRGRARWLTVPVIALWEAE AGGSQGE
12260	26161	A	12375	276	395	GHVVKTKKLKLIFFVFEMESCSVAQAGV QWHDLGSLQPPP
12261	26162	A	12376	295	472	VYSSVALNTFTLLCNHHQPSPEVLTFP NKKCRGAILAHCNLHLLGSSDSPTSASR VAG
12262	26163	A	12377	390	511	PGAVAHACNPSTLGGRGGQITRIPSL
12263	26164	A	12378	417	511	AHRSFFEMESCSVTQAGVQWRRLGSLQP SPP
12264	26165	A	12379	133	406	KLSLNKRDKYKQVCKETKKKKKKKKKK KKKKKKPGAKKKKSGGSPR
12265	26166	A	12380	247	345	HMWSSQLNKGLINKKKKKKKKKKKKK KKKKKKKKG
12266	26167	A	12381	156	15	NFFFFETESCSVTQTRVQWFDLGSLQP GKQEQNYVSKNKQKELIH
12267	26168	A	12382	275	1	KIVFLKGPPPLFFFFKKKFVFFLKVGFKG GLNFIKTFFPGGKPKISKRKQIFFFFFFF ETEPHSVARLECSGTISPHCNLHLPSSN DSLASTS
12268	26169	A	12383	43	379	LLGYDESRLSWICLCLSLGQLLSFLN LLVYVFCQTCEVCFHYFFQYFSTLFLLT FWDNVNLNRHFGIVPQVLDLDFVFFSPN KEIFLGQLQWLMPVIPAWEPEAGRSPE
12269	26170	A	12384	303	1	KGFFFFFFGLSPFFFLKKVFFPPFFLRT PPFFFFFFPFFKNFFPPPKKKNPPFFFP PPPPPPPPPPFFETRSRVAQARMQWGD HGSPQPQPPGSSDPTRP
12270	26171	A	12385	141	1	KKEPLRAPPPQLFCFFYFETTPCSVTQ ARVQWCNLSLQPPPLRYK
12271	26172	A	12386	31	417	CRLADSPSPNDTGQDSRGRAGIKHIPPL KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKSGGA
12272	26173	A	12387	291	412	LSSEMLLFCFVYFLRWSFTFVAQAGVQW CDLGLLQPLPG
12273	26174	A	12388	310	1	MTPCPFLFFCPKKRKAGGGFIKKALFFN PQKEVFLGPPPKGPFLLGFQPTPPWGKK IPRLNPLFWRSSIFFFLDGVSRLLPR LECNGLISAHCNLRLLGSS
12274	26175	A	12389	117	2	KRNPQRGGPLFFFFFFFETESRSVVQAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQWHDLGSLQ
12275	26176	A	12390	117	319	SFLKKPKDSTKNLKLINFEKSGSGPKI TIQKSVAFIYPNGEHSEKKIREVITFTI AAKTIKCPPQA
12276	26177	A	12391	95	2	SKSWTSLKLRTLGLWARWLTVPVLPALWEA KAG
12277	26178	A	12393	127	395	IPGSQGFCLIKQSALHLLNKSSFSFLSF IETQSLSVTQAGVQWCYLSSLQPPPPRF KLRQKNRLNSGGRGCNKLRAHYTPGWV TERDS
12278	26179	A	12394	252	391	FFCFCFVLLCFEMESCSVAQAGLQWPG LGSLRQGFAMLARLVSS
12279	26180	A	12395	275	3	TFRLVILKKSKETVEINCLETKSHSVAR AGVQWCSQDWEEKAGFNWRPSKARRCP TSVLKCHLGWAQWLMVPVLPALWEAKAGG SPEVRS
12280	26181	A	12396	111	3	GNNVKIRGLRIRPLKGWACWFTVPVPAF WEAEAGG
12281	26182	A	12397	124	1	VSRGRTVHQEKPTERAASPRLECNGTIS AHHNLCLPGSSNS
12282	26183	A	12398	259	387	YQQESFSCLFIFIFLFFIFYDTESRSVA QAGMQWHDLGSLKPP
12283	26184	A	12399	103	1	KGRFFFFFFFFYETESRSVAQAGVQWRDL SLQAPP
12284	26185	A	12400	308	416	CGNFEKAGRVRWLTVPVLPALWEAKAGG SLEVRSLR
12285	26186	A	12401	92	1	HTWGLTQWLMVPVLPALQEAQVKGKLFEP SS
12286	26187	A	12402	265	388	GLSWLFRPRGHLFYFIFPETMSVSITQA GVGCCDLGSLQPP
12287	26188	A	12403	279	1	SLSSKMESGSLTFSTIDIWGIITLSCC PGHCRMFSIRGLYPLDASSTTSSSCNN QNSPDMGTCSLWSQLLRRLRWEDCLNTG GRGCSEPGS
12288	26189	A	12404	387	152	NPPPGFNFGGPLKKNFFSPRGEKFVFL KRPPPPPPPPPPPPFETESHSAQAGVHW RDLGSLQALKSFCDLVSAFKGF
12289	26190	A	12405	262	464	IIFHWLACTLVIHSSFDGHGLFLPLAVA DSAAVKHSCITSICLNIEYIPGNGIAGSC GISVLNFLRNC
12290	26191	A	12406	204	67	KCFGQAWWLMVPVLPALWEAEAGRSQELR SSRPAAWAKELLNNRTRAS
12291	26192	A	12407	134	1	IQRPCIQLFSTFFLILFYFIFTEIDSCS VAQAEVQWHDGSLQ
12292	26193	A	12408	145	403	TYMYSLINYKANSHTKVNKHNTARFL ESLLCAHPNPPIKLIISLLREKKKKKK KKKKKKKKKKKKKQK
12293	26194	A	12409	65	415	RNKRIISQSWNGPSRKQSSALLCGLGH LTSGVRARVSPVQGCVRKGGSGPSKP KKKKKKKKKKKKKKSSKKKKAQKGG ALKKK
12294	26195	A	12410	124	404	PWWEFLHHRNCQMWPGTVAHTCNPGLG KKKKKKKKKKKKKKKKKSSSSSS
12295	26196	A	12411	164	2	TGAGLTIMDMVGVPDLLQLRFVFLFC FLVFFFETESDSVAQAGVQWCNPSSL
12296	26197	A	12412	114	3	PGMVAHACNPSTLGGQGGWITRGQVYKT GLAKTVKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12297	26198	A	12413	583	391	LADTGFHHVGGADLKPLTSCSTRLSLPK CWDYRCEPPLHLPVDPDTVLSTRGLISEKS FLPLCTFR
12298	26199	A	12414	280	2	KVSSMNAQTSVLFSTMLGISETLKYRGR KKRREREGREGREGRERKDECRKVRSER IEGGKKRGRKEYREEGRRRRIEVSANEET PRDHPANK
12299	26200	A	12415	264	352	RFLVHGCDIYICINIYTHTHTHSHTH T
12300	26201	A	12416	359	485	TDARMDWCYQEGTGSQAWLTPVIPAPW EAEAGGSFEVRSR
12301	26202	A	12417	171	1	PLFRWWGFELFPFPGYQKKKGYPFFFF ETEPCCVTQAGMQWYDLRSLQPPPPEFK R
12302	26203	A	12418	265	1	WHKSNEELAAEASAPVKARASNTILGPH THGKERCPVSLRNVLDEGVKSTNFFSFF ETDHSVTAECGSAISAHCNLHLMGSR DSGA
12303	26204	A	12419	278	388	SSLTGFFIRRRNEEPGQHGETPCLLKIQ KLAGCGVL
12304	26205	A	12420	205	413	WNLFVYLYQTHKYARVYSNIILFTNKK RAIGQAEWFTPIIPAVWEAKVSRLEPEVR SVRLSLPKWRITS
12305	26206	A	12421	103	2	RSLSKHRTETILGLPAVLIILFPPLLI PTSKY
12306	26207	A	12422	372	478	NIFVFLKETPCQSQWLMSVIPTLWEAEA GGSLEPR
12307	26208	A	12423	174	416	KMHYCVLSAFLILHLDTVAILSTCSTL DMDQPMRKRIEAIHQQLSKLKLTSPPK NYSEPEEVPPEVISIYNSTRDLLQE
12308	26209	A	12424	572	733	RFSCSLSPGSDYKNCNLSGSRGYSEPR SHHCIPAWVTEQDSVSKQNKTKQSA
12309	26210	A	12425	123	2	GYIFIFYFFETGSCSVAQAGVQWRNLG SLQLPPSSSDS
12310	26211	A	12426	224	417	TADFYGVNYISIKLLPKKKKRGPFKE SKFTAAGLQKNIFFLSAPNFIALAVVLK RRDWETPG
12311	26212	A	12427	115	3	FFETGSHPVTQTGMQWDCNSLQPLTNR LKQSSHLSL
12312	26213	A	12428	250	398	PWAGHLTSLGLSLPIFNIGIAGACWLM PVIPALWEAEAGRSLEVRSSK
12313	26214	A	12429	215	3	KKGLVVWGANKLWVFTPKFFLNQFSGW ALTPRGKSWFSKRRAPAPFFFFFFWETE SHSVAEAGMQWHDL
12314	26215	A	12430	345	2	FSHHPAKPQGGLFYRQPLGLEGKETRPR LNDRFMAGPSFPAQQLRMPFLGKEWER EGCSFVQCPVEGFAMWPYPLGSPGPRL FFFFFFEAGSPSVTAECGSGSITANCSL EL
12315	26216	A	12431	348	3	LYSSLGDRVKLRLKTKTNKWCLHSYIS TKIINLDHYLIPCTKTNSWIKYLNVR TNSIKLLEEDISVNLHELGSNDNSFLAMT PKAEIIKEKIYKLHFIKIKIFHVSIEDII EK
12316	26217	A	12432	160	52	NTAIGHPHQAIYLSYLSIIYLSIYLSIY LSIYLSIYL
12317	26218	A	12433	180	2	GRSKLHICREHSICATEHVCGCDTENNT NLCQVQWLMPVILAIWEAEAWRSPEVRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRA
12318	26219	A	12434	193	3	PGAENPPPKGGPPFFFFPRGFPFGVFF LKKKGFPFFFFFDTESRSVAQAGVQW HDLGSLQ
12319	26220	A	12435	321	422	NVEGDFLQRIKNIRYWP GAVAHTCGPST LGGRGG
12320	26221	A	12436	116	2	HDRFCLFVYDRVSTLSRPLECSSAISAH CNLR LPGSSN
12321	26222	A	12437	302	400	THTHTHTHTHTHSGLLYLPKGKQSH EFCW
12322	26223	A	12438	329	399	LALQARLECNGIISAHCSLCLPY
12323	26224	A	12439	310	2	KPILSRGLFCARPCFRSNMRSFNPSQS YQVGKDTFGFTVKVTKLVLGPSRGPKG ARQGVHKGKCLLTLPKMLRFLFFETES CSVTRLECSGAILAHCNL
12324	26225	A	12440	151	401	EGMPHLPGSHSSSNILKRGRESGREAGR KGRKERRKEGRERRRKEEEKRGRGKIRR RKDRGENEEENNRLSSKVSLEISTCP
12325	26226	A	12441	276	1	FHPFGRPSVSPRVQPKIGIIHTCVARI EKGGSCKALSLCPQYVGSNFFFFETRS FSVAQAGVQRCDLGSMQPPHFPSSDPP APASRVAG
12326	26227	A	12442	140	1	NSHFPPKNLGSPSSFFFFFYLETESRSVA QAGVQWLDLRLSLQPPPPG
12327	26228	A	12443	310	3	LPPCSWGLYGAFARCP LMDKQLSQVPL WACPLSTAGRTRLCVACIKAAAGKAQGGF FFFETESHSVTQAGVQWHDLSLQPPPTH AKPKHTHTHTQTHTIPTD
12328	26229	A	12444	337	2	GFFAIVPKKGQKKMFSPFKEGIFSGPC FISSTPTLLGVKKILPNTSEIRPVLSS IINTSVHIREQKKTYYVGIFTGKSRFFF FETDSRSIAQVGVRWRHLGSLQAPPPG
12329	26230	A	12445	112	9	GRVRWLT PAIPALWEAKAGRSPEVRNSR PAWPTR
12330	26231	A	12446	172	3	IPGELLIGRAKFAKNWPAPRGIPLGR QKFSFFFFFETESRSVAQAGMQWLNLS
12331	26232	A	12447	221	418	RKAERLEVFRRRLCQRALRPFPHCLAAA PMPLIVLKKPILGRAWLTVPVIALWEA EAGGWLESRS
12332	26233	A	12448	280	392	PLGRVRWLTTPVIAHWEALAGGSPEFRN LRPAWPDMA
12333	26234	A	12449	410	129	PSQEIFFYPGPPGKTPFPLKKKKKNRGG GGGLPFPFPQVKKKKFFYPGRGRFKQP KFNP LPPPRGEKKNPKPPPKKKKKEK KRKEKKLVT
12334	26235	A	12450	159	1	KKKRGFLGLTFIKKTGPDFFFFFETE SRSVAQAGVQWYDLGSLQAPPPGLM
12335	26236	A	12451	270	1	NPLKFFFSLFQNP LKKDPAIFNPFFFF FPRIFWPFFGGVSKAGIWWFFFFF FFFFFETESRSVAQAGVQWRDLGSLRT RGRTRG
12336	26237	A	12452	249	33	DKLVKLPLILKKLNSFFFFFETESRSVA QTGVQWRNLGSLHPPPGFKPNAWAYAW AHAWVVPGLPAQNLR
12337	26238	A	12453	190	86	TNDLGWTQWLTPVIALWDAEAGRSLEL RSTRKA
12338	26239	A	12454	318	2	PPTFPLKTLFFPVFLPKLFSTLFSPPKKK FSNFLVSAPPPFFLT L GNSQGVLLKGGP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFFFFFETESRCVSQVGQWRDLEKK EKKKCNNGGRHYISTHLKYK
12339	26240	A	12455	204	288	IQLNTHTHTHTHTHTHTHTHTNETGKMW I
12340	26241	A	12456	409	13	QGGAPPPIPIMLSFLQEAGLLHVAQPGVK LLTSGDPPSPPSKSAWRQRETRLNLGG RGRSEQRPPPRPAWATQQDSVSKTNKQ TKNNKKIRKSLCKTLEKEMLAVMIITK YLLCTDVPSTVLCTHLYYLT
12341	26242	A	12457	204	3	KKKSTPQSAKFFPLGGGVFFFLVGMRS PFVAQAGFKPLGSSDPPILASQSTAITG MNHHTSSAFH
12342	26243	A	12458	289	3	KAREKKKVGATKNIRIVDLKSGRTSLCK KTEMPVGNRNKQKPNPSNLRISTRPE TESRSVTRLECSGAISAQVILPGSSDSP ASNWRQSETLS
12343	26244	A	12459	261	388	SWHFGRSKQVYCLSLGVRNQPGQNPVST KTKISQAWWHAPW
12344	26245	A	12460	313	391	RVGRVHWLKPVIPALWEAVAGGSPEV
12345	26246	A	12461	112	7	HICIFYFFETESRSVAQAGVQWHDLSLQ PPPAFGK
12346	26247	A	12462	389	3	ALHEGAARGSPPPGGKKKKRGSPFFMGN QAPQVPGKLGGGGFGWFFKSLPLQPGG KPGVFYKPKKVTPKDPPTLWGGWGT TGGPPGPLFFFFFFFETESRSVTQAGVQ WRHLGPLQPQPPAHAS
12347	26248	A	12463	26	349	CIMIDSTTGIFHCWWECEMAHPFWKAV WQFLFFFFFFKRGVYFFFPGGIKGPGFGLR EPLPPGIKGVPRPNPLGGDLRPPPPPP INLGFPGKGVFMVWPGVGNFLI
12348	26249	A	12465	187	54	GYKNKPGQAQWLTPVIPALWEAKAGGSP EVRSSRPAPWPIWTRG
12349	26250	A	12466	199	55	I IQLRQQNSFLFCFDIESCSVAQAGVQ WHNLSLQLEVPGFKHAPSH
12350	26251	A	12467	107	3	FAHCLIGNSFFSFFFFFFFVGSCSVAQA GVQWSD
12351	26252	A	12468	120	1	GNWCRAQWLTLVIPALWEAEVGRSPEVG SSTRLGLPTHR
12352	26253	A	12469	105	2	YYLYFIFLFFLETGSCSVTQAGVQWKD LRSVTS
12353	26254	A	12470	238	405	FHICLFILKNQVSKMYHTVSCSLEI YCCLLQWLTPVIPALWETKVGGSLEVRS
12354	26255	A	12471	425	1	LNPAPALFFGGPKKNFFSPRGDKFFF FKRAPPPFFFFFFFQKKKKPFFPA QKKGRGFPGRALSQWPLAGFLKITQFPP WSRVFSPLLFFFDMESPSVAQAGVLW HDLHLPGSSDPPTPASRVAGITGVCHH A
12355	26256	A	12472	122	2	QNKYSELRMNTFGRPQWFTPVIPALWEA EAGGSPEVRSSR
12356	26257	A	12473	144	420	GAPRPISRPRGKTPGGGGRGKPNKNGL GENPFPFKGVKGNPPIFPFLQNGPT PLVLGSANMGFYLYLKRKGPGKGREALR AEPGQFFY
12357	26258	A	12474	80	1	KGGQVQWLTPVIPAFWEAEAGGSPEV
12358	26259	A	12475	54	294	LIKSWQHRQEYVSLMSFIFPCHIWYQS QRSPGTTQIILEISDTGKNKYFNCTGSH RKHTHTHTHTHTHTHTHAHTTL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12359	26260	A	12476	364	234	BEMGFHHVSDDDLNLSWSACLGLPKCWDYRSETSRLASLPF
12360	26261	A	12477	288	450	PGTVAHACNPSTLGGPGWSRTPGLKRITICLGLPKCWDFRRELLPSLPCLLIIFL
12361	26262	A	12478	271	396	TISFLSFFFLFLFFFFFWRKSGRESRF SQKKKKYKKKNIIY
12362	26263	A	12479	289	2	GSCLLERKLTyrKDIHTKNPSVPHHHQR PKVDKTPKTGKKQGRKTGNSKNQASPP PKECSSSPATEQKWMENDFAKLREKGRF RSNYSELQEEI
12363	26264	A	12480	323	1	YSMVYPYVFLTAKKDQLQVNNLTQLTCKS YQLYHCINHSTLQTHNISTLMILGHIPG LCIPVNLSEAWAATPALHFVKLLLTTELT HHVCRALDIIILAIVSLVALITS
12364	26265	A	12481	279	429	MNGQRKCVVYTLYTYTTEYYSTLKRRK WPGTMAHACKPNTLGGHGGWTA
12365	26266	A	12482	308	423	LTFKNTTGFFFFFTEFECFVPQAGA QGGDLSSLKAP
12366	26267	A	12483	272	474	MVSWGLSRKIPWVLSFFFFFEKKSHFF FQGGGRGGDLSWEQPLPRSKGFSCFTL PSTRDYRPA GP
12367	26268	A	12484	84	229	LFKSVCHLLPLSSCSSHVRQACLPTFC HDCKCSEASPAMPLPVQPAEL
12368	26269	A	12485	392	3	TGKKKRFPFFPKKIFNSKPKQFSWRKKK LFKIFSPGGAPFPFGVQKKKTFFFYP FSPRTFFSIFFPKGPPKGGGLGPPFF POKRGGGFNSKWETWEKFPPLFFFFF ETESHVAQAGVQWHD L
12369	26270	A	12486	76	1	KLISWTWWHMPVVPATWRAEAGDFS
12370	26271	A	12487	204	8	FFIFFFFFFFFFCKTGSHSVQAEQ EWHDHGSLQPPQSFHLSLPCATMPGL FFLFLFLT
12371	26272	A	12488	96	3	KKPLGQAMFFFFFFETESCSVAQAGVQWC DL
12372	26273	A	12489	126	1	KPPHPFLPFFFFFFETESHVAQAGVQWC YLGS LQAPPGFTP
12373	26274	A	12490	107	2	IAGRAWLMLAIPTLWEAEAGGSLEPRS SQPTCAT
12374	26275	A	12491	302	2	GGFGFPREKGGFFQTVLFGVPPGFFS PPVFKTGPVFFLGAQKKIFFPPPGGK IWFFLRGAPLFFFFFFFEMTSCSV AQAGLQWCDLGS LQHP
12375	26276	A	12492	248	398	PTEQVTLGITAQSYSRVHINNRRVYDLAV GSGHPDGA A I KGSFVQRLKSY
12376	26277	A	12493	341	1	KTSHFREIYPLEHASSLSKKIETGALPC SQELLNSQENSVMNKFPCLNQLPFQDVN SCIIRFQTKDTLKHTAIQPEAKTSLPC YTHTHTHTHTHNNHSIFELLCMQCDSY N
12377	26278	A	12494	95	3	PLFFFETKSCSVQAGVQWQNLGSLQPP PP
12378	26279	A	12495	62	420	CAAKLCTEAHTAASADTHTSPHGSVSGL FCFHFPPhRRQRSRPGKPGAHRLAGR ALSQKPVGSGATPHNLHQIRTQTNGLI QLLGDRQAPWVTPVLPVLWEAEAGGSLE ARSLRPA
12379	26280	A	12496	58	492	NSPPPPAPSQRTSPPA A A SPTTGSSSA PCPASSWPRSSIALITFYDPQPCGLSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NNLAWKQNVLCFKERLLEKMFRRIQVLG LLVWTLIAGTEYFRVPAFGWVMFVAVFY WVLTVFFLIYYITMTYTRIPQVPWTTVC LCFKR
12380	26281	A	12497	2	198	RLQGILSAGFLVPGDTSVSSPRPRAAGS QSSTSRVLWKLSGAMLRLYLVMGVSAF TLQPAHTG
12381	26282	A	12498	71	346	GMFMTSKETFTHYQPOGNSDPAHTATAP GGLSAKAPAMTPLMLDTSSRKLVAWDGT TDGAAVGILAVAADQTSTLTTFYKSGTF RYEDVLWP
12382	26283	A	12499	122	59	HQIYIYIHTHTHTHIYIYIYI
12383	26284	A	12500	220	3	PKKESVRCVAMKWLILLCLQTSLSHWSL PQSSLAATPCCLNLGTVDVLQGLGAVAH AWNPTSLGGRDGWITS
12384	26285	A	12501	125	1	HVLVLSHFLFVLFLFFETESRSVTRPKR SSAVSAHRNIRLS
12385	26286	A	12502	373	476	ILTRDGVSLPRLECSGTISAHNLCCLL GSGDYP
12386	26287	A	12503	440	573	STWEDHLSLGNRGCSPEIRLHCTPTWVT E
12387	26288	A	12504	146	5	HPHLQTMNGAPIPQELTFLLEKERDGLR CRGNRSPVPGIIPRWSRDL
12388	26289	A	12505	140	44	AQGLTPVIPALWEDEVGRSPEVRSRSD WPTR
12389	26290	A	12506	247	420	LEISVTFSCSFGCLPKKHITHTHTHTH THTHTHTHTHYIRTITYTTLARPLSALH NF
12390	26291	A	12507	346	473	KAYIIGLNCFYETKSHVAQAGVQRDL NSLYS
12391	26292	A	12508	87	414	RTGVYRVGKDGRSRSPDLLICPPLGLPK CWDYRREPPRPACPLLSHPSPPHFSF LSPFLSFLPCSPFLYIFFPPPLPISL RWRLIPEGRFMAPLCLQMPGLGHT
12392	26293	A	12509	386	467	LLLFFEMESHISITRLECSGAILAHCNL
12393	26294	A	12510	344	472	KFLFPDPAVSLGLIYPKESKSFYQKDT TRMFIALFTIANTW
12394	26295	A	12511	424	132	RGEGPPRSGILSPVGPGETPPFLKKQK ITRGGGGPLFPPLKRVGENSFPPGK SFHGAKFPFCPPPWATKRNSVSKKKKQ TKKGSRIILYNNE
12395	26296	A	12512	351	510	GGTDFCKQSKLQSLQPAVEIFIPGRVQW LTPVISALWEAEAGGSPEVRRSRPA
12396	26297	A	12513	362	463	NTITWLGAHAACNPHTLGGPGGRITWG QEFETS
12397	26298	A	12514	137	1	EEISLLLPRLECNGAITAHNHLHLPCSR NRRPGKAVHVRQAYSFQ
12398	26299	A	12515	251	592	GAFTGLAFTMAGGRPHLKRSFSIIPCFV FVESVLLGIVILLAYRLEFTDTFPVHTQ GFFCYDSTYAKPYGPEAASRVPPALVY ALVTAGPTLTILLGELARAFFPAPPLAG PV
12399	26300	A	12516	3	413	SWGGRKFLCPPRSLSGSRELHPAQGDRP GPLSSSGKRETGTHRETLGKKKVSSAPE AQQAGLRLSQALGGLCYDLSPLTEPRLP LAATAFPRPCPALPHQPQVPTMGSVSSL ISGHSFHSKHCRAQNKLRKSSHLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12400	26301	A	12517	115	2	KSHGGHGVFVLVSVLVGLAMEVGLVLVW KEYDGAALA
12401	26302	A	12519	444	34	YCLRQKHTEYRRRSNLEMASSCLSGRKT CTFFFTLYQNLKMIKLSEGTWQAEWLKS RPLAPNSKVVEAKEKFLKKIKSVTSLNT YILRKPNSLIADMENILVIHIEYQTSYN IPSSQRLIQSKALCLFNYLEMECRI
12402	26303	A	12520	1088	935	ILTIIFINRCEFLRSKSSSEITQYIQS YKGFVDRTVMYNSNFFLKFLDYL
12403	26304	A	12521	2	347	AMAAGSRTSLLLAFALLCLPWLQEAGAV QTVPLSRLFDHAMLQAHRAHLAIDTYQ EFETIYIPKDKYSFLHDSQTSFCFSDS IPTPSNMEETQQKSNLELLRISLLLIES WLE
12404	26305	A	12522	50	205	VVGESDRQSSGFWASSAHACNPTWEVET GGSLEARSWRLQCTMFASVKSTRP
12405	26306	A	12523	105	2	REVCSTIKVLRDLSSDRSNPGRFLSTSN SSLYER
12406	26307	A	12524	279	455	KTKNWLALGGPPCFPGQYGETPSLLKNE KLAGHGGAPLYSRLRLRLRRGNSLTPGD RGC
12407	26308	A	12526	305	454	LYFLLPFQIINRMVLFFVFCFFFETES HSVPQAGVQWRDLGSLQAPPPG
12408	26309	A	12527	363	459	CTILGQAWWLTVPILALWEAAGRSPEV RGSR
12409	26310	A	12528	182	36	QHIVVFHKEHGQVRWLTVPVISALWKAEA GRSPEVRSSNAAWHACRNSA
12410	26311	A	12529	388	530	KSFNLFFPRDGLNCVPQAGLELGSSDP PASAFRVAGTTSVWHHSQI
12411	26312	A	12530	134	1	GHKKGVLFFFKTESRSVAQAGVQWCTL GSLQPPPLPAHATRPV
12412	26313	A	12531	230	1	KKFGFFPQAGPQGGHLHFTTLPAPWGQAI SQKREKPPFFFFFETEPHSHVARLECSGT ISPHCNLHLPSSNDSQASTS
12413	26314	A	12532	145	3	KKLEILSAIIPPKFRKEIFLFFFYETES CSVAQAGVQWRDLGSLQAP
12414	26315	A	12533	365	2	LEFFTSLIWQITLGFILNCPGPIGVCI YIQFANTFRKFAFLFTNEIAYNILILPL TKQDYTNLIKLIKHSFFSNFLKQLLFV FCFVFSLSLFAMESCSVAQARVQWRNLGT LQPPPPRFK
12415	26316	A	12534	313	475	FFWSCSSFQQGFGGGITTIIILRWILA LSPRLERKWRDLGSLQSPSPGFKRFF
12416	26317	A	12535	124	3	MGSLIMGAELSVYRQVCDCKPQGVCVCL CVCVCVCASTCM
12417	26318	A	12536	333	58	ACNPSKVRSCRPAWSNMVKSCLSKNAKI TKEWWANFFVFVFLVEMMFHHVQGSL LKLLTSSDLAASASQSYGITGVNHYAQ PARTRGSR
12418	26319	A	12537	214	3	SDPRRACRCPKEAPEQQRRPLPGGSVPAL SIFFFFKTESCSVPLSPRLECSGVISAH CKLRLPGSCVPAS
12419	26320	A	12538	146	1	MNFLAFTNPPRPPQILKPLLFILRES HSVAQAGVQWCDLSSLLPPA
12420	26321	A	12539	195	1	IFIPPQAQKRGDPFLSFFFETRSPSPR LECSDAITAHCSLHLPGPGEPTTPPIPK SWDHSVPP
12421	26322	A	12540	151	334	LLGLRLHKNHNLNPGGGGCSGTIMALCNI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLPRSSSSPTSASKVAGITGACHHACCLRYFLY
12422	26323	A	12541	314	402	NLNSGPAWMLPVPVLPALWEAEAGGSPEVG
12423	26324	A	12542	339	3	GSCLLLEGKLPNRKDIHTENPSVHHHHQRPKVDKPTKMGKKQNRKTKNSKTQSVSPPKERSSSPATEQSWMENDFDELREGFRRSNYCELREDIQTKGKEVEIFKKNFERV
12424	26325	A	12543	31	365	RSVAVMPTEDRATWKFNYFLKIIQLDDYPKCFIVGANDVGSQMQIRMSLRGKAVALKGNNTMMRKAIRGRLENNPALEKLLPHIRGNEGSVFTNEDLTEIRDMLLGKVV
12425	26326	A	12544	278	410	FSFKNVTAGRVWMLPVPVLPALWEAEVGGSPVKKRSRTTLANMVK
12426	26327	A	12545	88	276	EVPPQAHKRLPSAPQLRPLQAISTKGPCPPQSPQSPRPRPEGSSAHSRGEKRTREGRKEEKKKKK
12427	26328	A	12546	251	3	PVEDNSKRRFQTGEEKVTQEEQALTPWRTNFFCFSDRVSAQARVQCDSGSLQPQLPGSSDLPTSASQVAGTTGMRHHAC
12428	26329	A	12547	106	2	DEHLFPFLTSFETESCSVAQAGVQWRDLGSLQAPP
12429	26330	A	12548	225	1	GFFKKKEPHPRPCKKKTPPKLKPFWGGLNKKIPLSFVFSKKGPLPKKFFPPPPFFETGSCSCHPAGVQWCDHGSLQ
12430	26331	A	12549	218	3	VPPPGLVPGLPQIIPKGFPKTKGPPKGPVPGDKQKSGPPNKKNFFFLRRESHSVAQAGVPWCDLGSLOP
12431	26332	A	12550	276	24	GPLKMVEAPPQNPLSPKNKIFPPPPFFETESHVAQAGVQWRNLRPLGSSDFPASDSRGAGITGARPHVQLIFVFLVKTGRKRR
12432	26333	A	12551	331	440	KSASSWSFNKSGWGWLTVPVLPALWEAEVGGSLVR
12433	26334	A	12552	136	1	RHTGSKTTATALVDVFLLLFFETESHLSRLSCSGTTPGHENLYE
12434	26335	A	12553	84	1	IFFCLFSFEMESHVAQTGVQWCDHGSL
12435	26336	A	12554	3	349	HASGPEELSKDPSLVSQGQPHRKPGLKRCSSRPLGPPDKLGGEGKQGLLGFTLWLSGPIKPCDDEEKNNKKKKKKKKKKKLGGGPFKKKLFFPPGGGRNFFFLGAPKFFWAGRF
12436	26337	A	12555	257	417	KQLHLQGRFLFSPSFLPSISKLFFFEMESRSVTQAGVQCDLASLQAPPFGFT
12437	26338	A	12556	268	403	YMRLSFQDLVMPKDVAVDFSQEERWECLNSYQRNLYRDVILENYSN
12438	26339	A	12557	286	426	DMLIKTCCHLVCEKKKKKKKKKKKKKKKKKKKKKRGALKKKPLPPP
12439	26340	A	12558	114	1	PLKEIANRHMKKCSSSLAIRQMOKITTMRYYPVPTMA
12440	26341	A	12559	106	1	FFFFFFFFFFFFFEMESRSVAQAGVQWCDL
12441	26342	A	12560	118	2	KNYSNNLKTNAGRAQWLTPAIPALWEAAGKSPEVRNW
12442	26343	A	12561	196	2	MCCFSKNWQEGAQMTPGFEPQDNSEKTKLSDTRLLFFFFERESRSVAQAGVQWRGLGSLQAPP
12443	26344	A	12562	128	3	RAPPPFFFEFETFRSLPRLECNCAISAHR

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLPADFYSATSQTKPDILQSMQKAFKNS GIGQAWWLIPAI PAALWKA EVGGLLEPR NLRPAWVYGKTL SLQK
12467	26368	A	12586	76	379	PLHPPASCPAPSL SCLIPGSPSDPLFSD SARPGWGRGWGRAPQLPPSPFFLYNLIK KWSRFCHQKKKKKKKKKKKKKKKKKKKK KGFFFWRAPFFFFFGGFFS
12468	26369	A	12587	109	376	LEFFFKMSGVVPTAPEQPAGE MENQTKPP DPRPDAPPEYN SHFLPGPPGTAVPPPTG YPGG LPMGYSPQQPSTFFLYQPVGGI H PVR YQ
12469	26370	A	12588	323	1	KKFCPPRFFPFLFGFQKGTNPISPFSG GFKKNLGGFNPPRPWPSPQIGFFLGRS KELILGLFPTRIGIGGFFSFFFFCETKS HPVMRLECSGVISAHCNLRLLVS
12470	26371	A	12589	262	1	GDPPTTSGPQTNPQKEHLMNFKSDSQLY EDTLAGRSVLINLTPQTLQPRWTGPYL VIYSTPTAVRLQDPPHWHRSRIKLCPS EKK
12471	26372	A	12590	284	374	TESRNWGWAWLTPVILPALWEAEAGGS PE
12472	26373	A	12591	297	387	GQAWWLTSVIPAFWEAKEGGSPDVRSSG LA
12473	26374	A	12592	206	407	VKPQNPRKAQKLKGLVYIHIYVYIYVYV YIYIYIYMYICRYISLTVVYTVNSKEKG LDTAAHTCNSR
12474	26375	A	12593	222	379	LTTGSI MGNFSLILVYTRKVMGSVQWL TAVIPLLWEAEAGGSLGRSSRPA
12475	26376	A	12595	301	189	KKIQSQAQWL PPIIPALAEAGRSLEL KNSRSAWAS
12476	26377	A	12596	209	3	SVKPLFFINYQSQVVLFLFFRGR LKRS TISAHCNHLPGSRFSCGLPKCWDYRC APPTLKIDLTKD
12477	26378	A	12597	306	3	NGKKGFYMAPEPPFFHFFFSPLFPTL FFFFIFPLPFCFALSFLVGSSSLSPRL CPMQHYFCDAWNTFDALIVVGSIVDIAI TEVNVSTWRLSLTVRV
12478	26379	A	12598	1	249	NTGAQCPLFESIQLQLFLGGGEDGVS LLLLRLLECNGAISAHCNLRFP GSGDPPA SASRVAGITGACRDHTCEPPRPVPPSS
12479	26380	A	12599	228	404	RLSSLSPVTEFGCLSPDLILKCDPWP TVTHTCNPSTLGGRGWITRGQEFKTSP VNM
12480	26381	A	12600	101	580	LSLTKNCALLGEETMMEQEMTRLHRRVS EVEAVLSQKEVELKASETQRSPLQDLA TYITECSSLKRSLQARMEVSQEDDKAL QLLHDIREQSRKLQEI KEQEYQAQVEEM RLMMNQLEEDLVSARRRSDLYESELRES RLAAEEFKRKATECQHKLK
12481	26382	A	12601	464	3	CAIQOTLYEHPMKSSRLGPTQLKIFTCE YCNKVFKFKHSLQAHLRHTNEKPYKCP QCSYASAIKANLVHLRKHTGKEFACDY CSFTCLSKGHLKVHIERVHKKIKQHCRF CKKKYSDVKNLIKHIRDAHPQDMYCGR SRGSARMSRALPS
12482	26383	A	12602	140	1	WIGSFLSSEEDGTVVQKISGVQRSLSLY VYIHTHTHTHTHTHTHTV
12483	26384	A	12603	112	2	ESLRPGAVAHTHNPSTLGGRDGWINKDK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EFKMCERV
12484	26385	A	12604	139	1	KKRVKRGPPGGFKGLGGKFFSPKTF FFFETESCSVAQAGVQWR
12485	26386	A	12605	204	460	SGQNGEICHPRGFCTLPKAISLLIAR VCLKHFNKGVASLSQTANGCFFEGFSET ESRSVIQAGGQGGDPGSLQPPPPGSCLS L
12486	26387	A	12606	317	1	KRPLFKNIFQKPPFFKNGAPRKKGPRCIF GPNQKNPLFFPAPLSPFWETKKGAGFF FWGFFPPPTKIIGGQKVPFPPTFPFFFF FFETESLSVTSLECSGAI SAH
12487	26388	A	12607	248	367	TQILSSGSGVQSSLHHPPICFIHTHTHTH THKHKHPHS
12488	26389	A	12608	2	387	QKQQQRAGRETSTCSLRIISAPTMAFV ELSTKAKMPIVGLGTWKSPLGKVKEAVK VAIDAGYRHIDCAYVYQNEHEVGEATQE KIQEKAVKREDLFIVSKVQWCIWLAFNT IVPKSQWQSLQTPQRC
12489	26390	A	12609	258	23	MWERGIIRPQTQTLTGEPEGLDHGRSIS PNSVMNGIVPHISILTNLINGLNAPLKR PGIAEWIRIYQTSMMCCLQETGR
12490	26391	A	12610	176	433	DALSSAWGTVLGTQIPSHFTEILMLSP AWGSSSLTQTLFYVPSCAKRTGSYVLAR VGQKYKTLWLGAHAACNPSSLGGRGRW IT
12491	26392	A	12611	312	410	AHMYRTCSRGWVSWLTPGIPALWEAEAG GSLEP
12492	26393	A	12612	3	289	VFEFLSRKLSYILRMFWTFKEFWLERF WLPPTIKWSDLEDHDLVFPVKPSHLYVT IPYAFLLLIIRRVFEKFPVASPLAKSFGI KETVRKVTPNT
12493	26394	A	12613	294	432	FMKLLLLFFFFERRRSCFVAQSGMQGGYN ASLQPLPFGSSNFGSLPL
12494	26395	A	12614	138	375	SPNATCGHADPLPLCCLHICQALKRFT QTTTTFEGKPYLGILLYAVFFFLRLESCS VAQAGVQQPNLSSLETPPPSA
12495	26396	A	12615	232	1	GVPQRAKLRLAGLCPQAMDTFSTKSLAL QAQKKLLSKMASKAVVAVLVDDTSSEVL DELYRATREFTRSRKEAQKML
12496	26397	A	12616	236	419	LEMNRGWVWFFPPVNPWLWETEGVRDQP GQHEETLSLKIIFKISRHGGMRLGSQLL RRLRQ
12497	26398	A	12617	197	1	LCHSEGFLSRVSALLFTLLLLVLMESP PSVSQPGVQWPHFSSLQPLLPRFKQFCN TLP SGWDYK
12498	26399	A	12618	132	3	NSFMFHLFTYFEMESCSVAQAGVQWRDP GPLQAPP ERVGGRV
12499	26400	A	12619	255	2	MNSLNSFTDIAVIPLHYNRILPHFKIIL SYFLKSKFQVKGIGRVKWLTPVIPTLWE AEVGRSLEPRNCPAHQPGQYKGKILYKK
12500	26401	A	12620	141	2	FHFTYIIITSCVCVCVTSRFRVARLECSG AISAHCKNHRPGSSNSPA
12501	26402	A	12621	274	421	TYVMEVCCTYYFLAQVLSLAPFNYFIIR PDPRTDPRDPDPDPDPPEPRP
12502	26403	A	12622	132	2	NQSIKKKIELQGFQSRSGGRGKGQVWL T HIIPARWEAKVGRSP
12503	26404	A	12623	390	86	IFPFFYQNTNGMAPGNQIPQGFSSRFFF FLRQVLALWPSLEYTGETDQCRLKCSS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLSLCSSWDNRCAPPLVNLIFYVETGS HYVVHIGLKLHLSRYPG
12504	26405	A	12624	297	396	IIRVRGRAQWLTPVIPALWEAKAGGSPG VRKSR
12505	26406	A	12625	303	381	KFHLVPSINTMSGSQELQWMVQPHFL
12506	26407	A	12626	318	152	GDKRRLVSKKKKNLWNFGRIQWVPPVIP ILLEGEGAGGSPEVRSFRPTGQQSMTPF
12507	26408	A	12627	48	388	QLGNGKVRLLYQRHSSSSFFFWGEGFPP GPQGGGGPNLGPRESPPPGVKGTTPPPS LLEGGEPPGPPPPGPNFWGFWKKGLPL YPGGPPTSGPKGEAPPTPPKGGGGIKGL P
12508	26409	A	12628	116	3	KVAINQAQWLMFVIPALWEAKAGGSSEV RSSRTADAW
12509	26410	A	12629	227	400	VLFLVLFCKEWHVFIFLILPVYSYKKKK KKKKKKKKKKKKKKKKKDSQKKD
12510	26411	A	12630	182	3	TNWLFPFPKFGPVPLFPLPPFFFFFET GSHTVAQAGVCSGAILAHCNLRLPGSSN TPA
12511	26412	A	12631	134	473	ASTIMDLLFGRRTPKELLRQNRALNR AMRELDRERLKLETQEKKIADIKMAK QQQMDAVRIMAKDLVRTRYVRKFVLMR ANIQAVSLKIQTLSNNSMAQAMKGVTK A
12512	26413	A	12632	100	462	QLLLCCCCRQWTA FNVPASPAPPPAWA HMAPSLLEPPSLLVTOICKLSAFSGPSI NAFLLSKKKKKKKKKKKKDRGGAPLKK KK
12513	26414	A	12633	313	441	CWELLKWLVCFLCHIIKTNNCWAQWLTP VIPTLWEAEVGGSL
12514	26415	A	12634	129	400	VSQCCWPTPPALYSISRQALAASPQGRP WDLQPTMPESPLLPAPAPWPKPLRRAL PPAPRCLGPSTAQGLRSAGAWCGTGRHL HLRPQC
12515	26416	A	12635	308	399	EIRGWTQWHVPVIPALWEAEAGGLPEVG SS
12516	26417	A	12636	285	390	IFGVLINSFIYFETESRSVVRAGVQWRD LGSLQPP
12517	26418	A	12637	260	2	GQGPFFFGGRGSPKKKPKLKGFFLVGGS KTQFFFPKPKGPFVFFVFFSQTSARS VTRLECSGMILAHCNLRLPGSSDSPASA SR
12518	26419	A	12638	76	3	ALQVQWLMFVIPALWEAKAGGSLE
12519	26420	A	12639	219	484	LGLQEPDLDEKPILELPLAELAQQLQTE ELSLESILCSYLKQALKVHQEVNCLMIF LGECEEBLLALKKLKKSERGLLYGVPM LKDT
12520	26421	A	12640	33	462	EGLSWG YREHNGPIHWKEFFPIADSDQ SPIEIKTKEVKYDSSLRPLSIKYDPSSA KIISNSGHSFNVDFTENKSVLRGGPI TGSYRLRQVHLHWGSADHDGSHIVNGV SYAAELHVHWNDSKYPSFVEAAHEPDG LAG
12521	26422	A	12641	2	414	SGPAAPATPMSIFPELYFNVDNGYLEGL VRGLKAGVLIQADYLNLEQGETLEDLKL HLQSTDYGNFLANEASPLTVSVIDDRLK EKMAVEFRHMRNHAYQPLASFLDFITYS YMIDNVILLITGTLHQRSIAELVPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12522	26423	A	12642	161	463	KEKARGRPKPLLLPITSATTAMGLTIS SLFSRLFGKKQMRILMAGLDAAGKTTIL YKLKLGEIVTTIPTIVFNVETVEYNNIC FTVWDDGGQERIRPLWN
12523	26424	A	12643	124	2	TVFGGQAQWLMPITIPALWEAEAGRSPEV TSLRPAPWRTRG
12524	26425	A	12644	258	454	NRPELCDYQGLREDSKRKGEINQTACQF LWPRQKMSSQTKFKDKELIAEYEAQIK EIRTQLVEQ
12525	26426	A	12645	636	182	APLERPSMIPPRCSGGQPSDLRSSPAQG TERPALGDRKGTPIAEFGGAGRAEAPP PRGSRQRFQRRQTNAHTKRVTRLISA APARHSPAFTACRQVGRPLRSARRSGKK PHLTVWCPSFQDPIQDTTLQIILSL GGDTFSDFPCS
12526	26427	A	12646	199	414	IYHTSRSLDRKLRAQRYDELPHYGGMD GVGVPAVMYGDPAHGPPIPPVHHLNHP PFHAKQNYGAHAPHNP
12527	26428	A	12647	130	3	DRGFLCVHTPLKKKKNTHTHTHTHTH TNHTHSHHTHTTK
12528	26429	A	12648	192	443	LLLCWAQESLGTLGENTASSHTAGLEWE SPLFACWFFWGFCLFVWLFVWFEPKSGS VLTLECSSVITAHCSLDLPGRDPPASA
12529	26430	A	12649	393	179	LHSRVQRSGCFSCVSNVPTGGMHFTRS SPQSNQEADQARWLTPVILALWEAKAG GLPELKSSREAWATP
12530	26431	A	12650	263	2	KAPLLVYKWEPNPGGGNFSPGMGTPTNF GVRFGGETKELFFFFFFGTGSHSVIQAGV QLCNLDSLQPPPPSVKPSQYSWDHRKQS NTK
12531	26432	A	12651	355	111	QDPCFIRLHLPLSFLSVFLECTKISLLD WRMLFPLLDGPPHLALSSLVSPINTWNY SFQQLMMFRDVAVDFSQEEWECLDL
12532	26433	A	12652	271	3	RQLKNILIFFSHKNMLSIKHIIYNYTLF LKSAFIFNLETDHLNCFPGSISAKSYFI LFYFFETEPHSAQAGVQWRDLSTLQPP PERFT
12533	26434	A	12653	333	2	PPSPGVFGNPPSPGDPGLKTFFFPRGPP PRFWGGGFFILAPFPFGGLFPPFPLPP SQGPPFPFFFFFFFEMESRSVSQAGV QWRDLSSLQPPRARFSDSPLYFLEGR
12534	26435	A	12654	310	444	TYLSNIFYFILFLVETESPSVAQDGVRW CGLGSLGPPPPGFRFS
12535	26436	A	12655	336	411	DQPGQHGETPSLLKIQKLVECGGAH
12536	26437	A	12656	114	2	GIFFFFGLESRSVAQAGVQLCDLNSLQ SPPPGFKQF
12537	26438	A	12657	191	1	KNFILTFSFRGAKNGDVFFPPPGYIQTG ENFFFFFLKWSFTLVAQAGVQWNLSS LQPPPPR
12538	26439	A	12658	1	445	LRTGSEFSGRDSKGLAAEPTANFGLLL ASIEDQGAGGGGYCGSRDQVRRCLRANL LVLLTEAAGVAGVALGLVSEAGGALAL GPERLSAFFFFGELLRLRLMIILPLVG CSLIGGANSLDPGALGRLGAWALLFFLG TLLASAL
12539	26440	A	12659	2	224	ESTASRIAFEAWQPETLPKGLNYSGASP VVLNAVLPKKKKKKKKKKKKKKKKKKK KKKGGGVFKKKKIKGGGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12540	26441	A	12660	96	1	GLKDGGRGQVQWLTPVISAPWEAKVGGSP EVMS
12541	26442	A	12661	1	457	CWVHLQKGCHFTLGRHLHSGQAEALLTSQ TGRPGRGAPHIPDGAARQRRSSHPRRGG QAEALLTSQTGQPGRGAPHLPDGAAGQR RSSPPRRRAAGQRGSSPPRRWAAGQRLS SLPRQGGRAEALLTFQTGRPGRGAPHIP DEAAGQGGAG
12542	26443	A	12662	175	351	KGIFFFPSPWKAGGAIWFKGTFAPRGKG NPPPNPSGEGGPKKKKPGPQIPRGPPPLG PPV
12543	26444	A	12663	247	401	SSNQEPGCKGPCVLTNFYFILGRAWWLM PVIPAIWEAGTGGSPVRSWRPT
12544	26445	A	12664	152	251	RENSCCFIKKKKKKKKKKKKKKKKKKKK KRGAP
12545	26446	A	12665	2	365	APTRSRCLRHASCTACRTVSTDTSSLRR ADPKGRSALLADIQQGTRLRKVTQINDR SAPQIESKGTNKEGGGSANTRGASTPP TLGDLFAGGFVLRPASQRDVAGKEEFI LAPLWTVSP
12546	26447	A	12666	179	1	LELSKSGSHWMRHFSLRSFYSLISPQLN TTVWPTTITPILLTLFLITQLKILNTNY HLP
12547	26448	A	12667	279	35	NQAPFKARFFTTFKNVFLKEIKKKRCWS GAPPIIPPPWGGGGGGPPWGGNLSPPGP PVSTPFFNGAQKKKKKKDRYGGACL
12548	26449	A	12668	299	399	ISIKKQRKGPVQWLMVPVIALWEAKAVG SPEVR
12549	26450	A	12669	1	385	KMQNRGFFFLTFLALLGLTSGAAKKKNK GKKAGPGSKSPNWPWGPPSSKDCGGV FRKGTWGAQTHGIRGRPCNWKKEFEAN CKSKFKNWGAGDGGPGTKVRQGTLLKAP SIKQGETIRVTKPCT
12550	26451	A	12670	357	1	AGKIAKICPVSSMQAPTCTGFPVGGNDNQ GQAPDGGQFPPLQQNTSSPDFSNENSP ATPPEQGGQDAPPQLEDEEPAFPHTDL AKLDDMINRPRWVVPVLPKGELEVLLKK GIDFSKK
12551	26452	A	12671	107	373	TGNYTPLEDCAEQMRLIAQVHLLSTRV KQQQVKIKQLLQNEVQFLDKGDENTVV DLGSKRQYADCSETFNDGYKLRGFKIK PLLNP
12552	26453	A	12672	196	45	YLYFHGSRERLAKKYDKLFKECCIAD LSKYKENKVCFPPIYGRFLFK
12553	26454	A	12673	33	448	KEGAERAGAAAPVWSFLDRRDSARTRS GTSLSGADMGDMKTPDFDDLLAAFDIPD IDANEAIHSGPEENDVPGGPGKPPQCVG SESEHTASASAGDGPVPAHASDHGLPP PDISVLSVIVKNTGLSRAGWRPWWDV
12554	26455	A	12674	250	29	KKQTNMWQSPYEDYRIFYTTISSLYHLS IYPPIYLSIYLSIYLSIYLPHTLSIITD YVSILEHELRLPLWRIQP
12555	26456	A	12675	377	442	SDRQWWCMPVVPATWEAEAGES
12556	26457	A	12676	1	553	RIFPGRFRVVKLPSCPDAMPGRLLFWV AFCLLGADHTGAGVSQSPSNKVTEGKD VELRCDPISGHTALYWRQSLGQGLEFL IYFQGNAPDKSGLPSDRFSAERTGGSV STLTIQRTQQEDSAVYLCASSLATAWHS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLLPAAHKPHPSLSLQLLDTLNRGFSLLL PHGKQVDLDLSLSFG
12557	26458	A	12677	232	3	GWSSDCQQRARVIEEKHSRQKGHIAENP SVHRHHQRPKVDKTTKMGKKQNRKTGNS KTQSASPPPKERSSSPATCI
12558	26459	A	12678	134	3	IFIVEFGGKPFSCSTISLSQWLWCLFTG IGELLWGQVSTGTLY
12559	26460	A	12679	212	47	NGTHPHGYTLHTHKHTHSCAHTHTHTHS LLLVRSFLLPQKNTTISRSCCKLGKP
12560	26461	A	12680	224	2	MKMASFLAFLLLNFRVCLLLQLLMPHS AQFSVLGPGSPILAMVGEDADLPCHLFP PMSAETMELKWVSSSQCI
12561	26462	A	12681	35	397	KPLISQNKIHSVSSSQTFGFFFFFFFFFGE KKPPFAPRGGGKGGPPPLPPGGGNRAP RGEKKGKGGKPPKPNPGAFPPQKEKTPG GGGGKKKTPAPPTPKEVDQPLPRREQRG PGRLLPRGA
12562	26463	A	12682	188	514	HTTHLVYVLSMAAFFFFFFFFFEKNFLFAPR VEKRGKDLGSLKLPFGFRHFSGLTLQG SCNNGAPPPSPVIFLVFFEKRGFPLVGR EGLILPPLQAPFCISFRGAINGPS
12563	26464	A	12683	366	3	ISQTQTQWTDWVSELELQGCALHRDTVA IPQTRSFPPFLMISCMTLFSLQLQMDRAF PFPPTPTPTIQQISTSPATWPLTHLH STPGLSVEYSSNTHKSSLSPTSQWIRVD PMLASPTV
12564	26465	A	12684	99	1	SSCIRFFLEQAYGQQSYGTYGQPTDVSY TQACI
12565	26466	A	12685	247	31	FLKEKRNQFYLFIFQRWLDPNKPIRKQL KRGSPYSLNFRVKFFVSDPTKLQEEYTR WVYGYIFLENIVKTLI
12566	26467	A	12686	416	253	PSPMTIPVTGAPRDADLWSSSHAKMLAQP LKSDSDVEVRLGSSQIFLCWRPSFNL
12567	26468	A	12687	116	3	CLLGRMWWLMPVIPALWEAKAGRSLEVR SLRPARPMY
12568	26469	A	12688	380	1	SPSSKLGLWSKHVSPLLCIGVCPPPVVS MAELRQVPGGRETPOGELRPEVVEDEV RSPVAEEPGGGSSSSSEAKLSPREEDL DPRIQEELEHLNQASEEINQVELQLDEA RTTYRRILQESASV
12569	26470	A	12689	157	488	REFVSQGGSHLKAQVRLEALLLTIGTPP WAHLSILHMTAMGQRENKREAASSRIQV LLNHSQAIKQESIILFFEMESGVWPRLQ YSRMISASCTLFLSGSNNSPVSAPRI
12570	26471	A	12690	514	3	PSIRAGLLCGSAENATPFLCGITMAAGP LYTYPENWRAFKALIAAQYSGAQRVLS APPHFHFGQTNRTPEFLRKFPAGKVPF EGDDGFCVFESIAIAYVVSNEGLRGSTP EAAAQVVQVVSADSDIVPPASTWVFST LGIMRHNKQATENAKEECMRPLRVSSSLV GP
12571	26472	A	12691	304	4	AESLRVAHERLDTRSTSSDIFNFPQTQS NLEMNSEILESANYQSSTSYSINTELS LFSKVNGKFSTEFQRMKTLQVKDQAITT RVQVRNLVYTVKINPL
12572	26473	A	12692	221	2	VGPATRDLCFADEPVGGRQKQKQWWVL CLSPNRGLAGRPDTLHITCASAHMRHT CMHTRHAHAHVHTHCI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12573	26474	A	12693	3	205	YMLCSILSTQEAFTICLGEKFIYLFYTL FRDGVSLLLPRLECNGVILAHCNRLRGD RARLHLSKKQK
12574	26475	A	12694	233	3	TMGPAHLFKGNHNGGWLMYKAFFFLF FFKTGSHSVAQAGTIPVHCNLRLPSSD SPAPASRVAGNTNVPHTLY
12575	26476	A	12695	408	3	PAREMEKFRVCVRKRPLGMREVRGEIN IITVEDKETLLVHEKKEAVDLTQYILQH VFYFDEVFGEACTNQDVYMKTTHTPLIQH IFNNGNATCFAYGQTGAGTYTMITGHE NPGLYALAAKDI FRQLEVSQPV
12576	26477	A	12696	123	631	REAVQGGKSGGCGFGSRDSRSSGAVSAA VGDMGDPGSEIIESVPPAGPEASESTTD ENEDDIQFVSEGPSRPVLEYIDLVCGDD ENPSAYYSDILFPKMPKROGDFLHFLNV KKVKTDTENNEVSKNHCRLSKAKEPHFE YIEQPIIEEKPSLSSKKEIDNLGASDCW D
12577	26478	A	12697	429	629	LALLYPLKWVGKPVNFMEEDILGPLPPP LNEEEEEEEEEEEEEENPVHKIPDS HEITLKHGTKT
12578	26479	A	12698	158	404	LPILLSVERLVEIYAYTFIQDLFSASNIP YSSSVFRIEMDQPRTHSGPTTASNPA STNSSAPSATNSKQERSSSSLSKPS
12579	26480	A	12699	185	3	HRRPTISIPSSVIHPAMVRLGLQYSQGLV SGSNARCIALLRALQQVCPILLSLMTQP HLVY
12580	26481	A	12701	181	3	TVWASMFLSAALRARAAGLAHWGTHVR HLHKPDMQNGAGGALFVHRDPRENNRDT PCT
12581	26482	A	12702	373	1	ILVQERDSQVRVIRMIDKLVSSRDVRGRG VEKQMTDHRVIYSVRKLQKRITPEFIP SRTTPKLLFLLVLP SGKTPGHPVSSRTI PEPPLPTEPLERIEHPVP SGTIPKPPE PPLPIEPHETMY
12582	26483	A	12703	272	508	TKLGKKQNRKTGNSKQQSASPPPKERSS SPATEQSWMENDFDELREEGFRRSNYSE LREDIQTGKEVENCEDNLEE
12583	26484	A	12704	341	1	VPQHPRPLAPPSLGQSWPLMEGSRPR SSLSLASSASTISSLSLSPKKPTRAVN KIHAFGKRGNALRRDPNLPVHIRGWLHK QDSSGLRLWKRRWFLVLSGHCLFYYKDSH V
12584	26485	A	12705	187	365	WEPSCRGPSAFKPTRCQSYDWACMCGAE GRSAMEQPQEESEPEVREEEIEEMAHAE GTP
12585	26486	A	12707	238	596	LWLVRVKYSIMSGAALGLEIVFVFFLAL FLLHRYGDFKKQHLRVIIGTLLAWYLCF LIVFILPLDVSTTIYNRCKHAAANSSPP ENSNITGLYATANPVPSQHPCFKPWSYI PDGIMPI
12586	26487	A	12709	131	2	DRVSLSPRLCSCGTILAQPSRLKQSSHL SLTGSWDYTHAAPCI
12587	26488	A	12710	151	2	YRQGLILLPRLECRVMIMALCNFESPGL SDPLTSASRVASTTATCHHTC
12588	26489	A	12711	151	1	NFPEFDHFTVGCLRAGSSLIHYWWECKL VQSLWKAVWRFIKDLKIDLPLY
12589	26490	A	12712	28	411	RVVPPARPAGEPREPHVSWVMKLNPPQAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LYGDCVVTVLLAEEDKAEDDVVVVYLVLFGSTLRHCTSTRKVSSDTLETIAPGHGCCETMKVQLCAFKEGLPVFVTEKYFLLPRMYRYRCLYTYPSSAAV
12590	26491	A	12713	351	675	ENPRHTFIYSLPLGLQKHQVLTVDIGFGTAIMTVGKSSKMLQHDYRKRWILQDGRIFIGTFKAFDKHMNLILCDCDEFKRIKPKNAKQPEREEKRVLGLVLLRGEN
12591	26492	A	12714	326	457	ACSHHQKRSQAPPPAHLWPDPCPHGSLPLLNPSCNPGREVSPT
12592	26493	A	12715	200	1	TITKVCVFTRTCGLKGLMAKALFDQRKDRESETECQVWWTLPVIPALSEAEGGLLEPRSSRPV
12593	26494	A	12716	208	405	KKERENKKHTNKKGRKKMVHICQWHSSLHRKFQGIYRKTGTGTGWAQWLTVPVIALWEAEVGGPPEV
12594	26495	A	12717	157	3	AKETPTHKGSCKKKFFFFFETESRSVAQAGVQWRGLGSLQAPPGFTPCI
12595	26496	A	12718	1	472	SPAILPRLAILPYLLFDWSGTGRADAHS LWYNFTI IHLPRHGQWCEVQSQVDQKNFLSYDCGSDKVL SMGHLEEQLYATDAWGKQLEMLREVGQRLRLLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLFLFDSNNRKWTVV
12596	26497	A	12719	537	1	LHTMNGGNESSGADRAGGPVATSVPIGWQRCVREGAVLYISPSTELSSLEQTRSYLLSDGTCKCGLECPNLVFPVFNFDPLAVTPGGAGVGPASEEDMTKLCNHRKAVAMATLYRSMETTCSHSSPGEGASPMFHTVSPGPPSARPPCRVPTTPLNGGPGSLPPEPPSVSQACI
12597	26498	A	12720	369	3	AAKIIPATRKASLELELSPSDSTGGTPKATISDTNDALQKNSNPYITPNRYGHQNGASYAWHFEARKSQLKCMCEGSSHD TLQELTAHMMVTGHTKVTNSAMKKGKPIVETPVPV
12598	26499	A	12721	230	3	KFFWVLAGLTGKNSDASASLNQVHISPLLFSRHHFPFSLGPLSSPVLQGSKRQLLATLRALESASLSQHPHPV
12599	26500	A	12722	26	110	REQYAEGNMRGPAPGKKTSGLQQKNVEV
12600	26501	A	12723	224	1	WQNDQASDPPKYSFTSQCLS FARLARYGDVVFQIRLGSCPIVVLNGERAILQAMVQQGSAFADRPAPAFASFRV
12601	26502	A	12724	120	530	KKVARGSRSRERSRRRRSRPKAIT\NRT*GTRCTPRRWRSTVLGMRSCTRAR*QRSGLSRGHTRSAGLCDHGSVRAGSGDGDGTGGGDRRLGLGRDSLILLSSSQSAAFSSASGSSSFFSATQPLRMLLEYFWL
12602	26503	A	12725	434	222	KEEKSREGEVKEQD*EKDREEEVEKSRE/RRRRRRRRRRSEV*YRKGRRRREREDILVAERSHRSFRNSIPSTL
12603	26504	A	12726	268	370	SNILIHMESMFFFFGTIPSV*KNLBA*KTGPDGDFIDKLYITFRGELTTFPHILLH*FTEGAVLFNSFSK\AASITLTPKPNYDIMRKENYSPISSYIWNQCSFFLEQIFPLSFKLNCPLIIPH
12604	26505	A	12727	103	636	VCFISMKQPHGSRHPPCS/PPRPGS*VCQQSRPLGPQPSAFGQLA*HRRGLGLQG

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						PRSPMQPVPHGGRVSGQTLPGKPTPKRP PGPAPRHGGHSLK*LVCAQPPPRP*S *ASQAVFTLQVPGKPQVWTPCPVPVRAP TP\PLSNGGLGVSEH*DGH*QAPTSP* PRCQGGAGEGPQ
12605	26506	A	12728	1193	1638	GLGFAMLPRLALNSWPQGDPSVPASRAA GTRGVHRHTQLQVSFNYYKVLAMHSGSQ L*SQHFRKPRRSDHLRSGVRDQSGQHGE TPSL/LKNTRISWAWHTPLVPATREAE ARELPE\PGROKIASERPVKPICTASLG NTCETPPQKK
12606	26507	A	12729	304	101	RHLHWPCPSPLAPTPDISHCPEPPKSQT SP/CPGT*CLGFLKCPSSCHFA*K/PLH PSEPARKSLAPDTCF
12607	26508	A	12730	91	264	SQRTISGLRVKENLIFVMIMFPPIYSSQ TFWSQTFMLKIVFMGISISICYIL/NT EKNLGGWWLAPIIPALWEAEAGGL*L RVKENLIFVMIMFPPIYSSQTFWSQTF MLKIVFMGISISICYILKLRKI
12608	26509	A	12731	1026	406	LAHFRSQIFSFSHILVHFERMVNLNRYR LACVRRVFRFLHVLAYFGRIVLKRYRF LVHFRREVFRRHMLACFRMVLYCYFL VLRKILLIYVTFITYFRKVFLRHNFRLG GY*RKYFGYAPRWLSFFLYRCQCFHYF LFYLVLRHLQF/CCFVVSFCLFDFLFL FSAACVFSVLQIAIVMFPFHALQLFFF* VVLCSNRSRQ
12609	26510	A	12732	1508	157	QDVGGSGFKVDTHPRGRMASIFSLLTG RNASLLFATMGTSVLTGTYLLNRQKVC EVREQPRLEFPSSADYPDLRKHNNCMA LTPAIYAKLRNKVTPNGYTLQDQCIQT GNPGHPFIKTVGMVAGDEESYEVFADLF DPVIKLRHNGY*PQG*LKHTTDLASKI T\QQQFDEHYVLSSRVRTGRSIRGLSLP PACTRAERREVENVAITALEGFKGDL\A GRY\YK\LSEMTQDQORLIDHFLF\D KPVSPLLTCAGMARDWP\DARGI\WHNY DKT\FLIWIINEED\HTRVISMEKGG\NM KRVLRS\FCRG\LKEVERLI\QERGWE F\MWK*AP*EYILT\CPSNLGT\GLRA\ GVHVRDPQSFSQDPTAFLKILEKPRTPR KRGHKVVDIAA\VADVYD\ISNIDRIG RSEGEL\VOIVIDGVNLYVDCEKKLERG QDIK\VPPPLPQFGKK
12610	26511	A	12733	261	487	TGSETDCAKQASFLPREVPTVAEMKME LLKNKQFW\RGVVAHACNPSTLGGQGGW IT*GQEFETSLANMAKPHLY
12611	26512	A	12734	382	668	YKRITDIFVDSETHVILINKRQSCRIPG FIQLVQLISHQLAAPRDYTVSHSVAQAG VQW/RNLGSLEPLPPGFKRLCLS*HAL KNLSSCDTPPQY
12612	26513	A	12735	401	27	GDRAEESAEPRAWSHSDNSHRYTTLFIC LTHTHVHNPVHS\HHTHTHTHTHTHT TVSHRHTETPPLLLKQTGLKFY*NSRDD TPRSRPGSSGLQRLSSPPVPFPGTVE ASADFCGHDLLT
12613	26514	A	12736	202	182	KYLPFIINLITMNLFFETHSCSVGQA EVH*S*LKPMPPG\SSDSPASAFQVSGI

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12614	26515	A	12738	319	2	TGSPSSSWLIL*FFLKIGFTKKG QNTPPHIYIYIIPRVDAFLFLFLEMSYSVY VVAVLSPLYFVNKLALTLHCRALNLSFL HKIQEPS\LGSGSG\PLSCNTII*RLCL RSLHLVFRSLWILPICDSSSVF
12615	26516	A	12739	1363	2000	DRVFVIPGWKCSGTIKVHCSLDLPGSSN PSTSAP*VAC\ATGTYPPCPGLNFLYF* MEERGFTQVA\QAGSQNSWGSKPNGTSE ASPKVLGMNKP*NLPNPGRSILN*DGSI RYKDNYP/WEPPKRSYKCLRQKKS I*L SAGPRDYEASQPRKNYPISLLTFTCTSS LHFNPTELTCSSQLQKSIRRLKSEESC PPLPACSLKHTQAIKIF*RLHRTA/L FYLLK*NCFRN*S**KYFLSVSNLKI/ QWVRSSLHPGAPGYTPTV*RPKHKS NVL I*IQS/ITRCLFYILVYMRITFPLQLFL SKHPSTYKEDFA*VLPLSFFFFEMESRS AARRSLSSLQPLPRLKRFSRLSLLSSW DYRCAPPGLASPSILSS*GSCCSIQFIL RMSTISHAINVLVLKNTYLVLSASEHS LKKPC
12616	26517	A	12740	1696	743	GGQIMRSGVHDQPDQGETLSLLKIQKS AGPGGMHL*SQLRLRLRQENRL\NRGCS EPR/SRHCTPAWATEQDSVSKKIKK*KK *NHLESKQQQPALEPPEQAGGQLRKTE QLQDGRRELAADMTL*PGHSKRLGALPR PLLSAYYFNKVHAARRQAYLETPTGTFS YQREEGEQALILGVEAQASSPTVFHRER RQSQALCSHRKSQEAPVRPAHPRRVPG LGKPSSQGLSAHLGQDRAPAPRRASWDQ RSQAPISVTFPSVLDKESVPCGPGFPG HAPAPRGIHGATWEGAHSRGYPGHFLAL PQHNSDEQRPN
12617	26518	A	12742	2473	445	RGARRRRRRSRHRRRRHQSRPVRAAPRQ PEQRRRGAPTHGPQLIMMDLELPPGGL PSQQDMDLIDILWRQDIDLGVSRVDFD SQRKEYELEKQKLEKERQEQLOKEQE KAFFAQLQLDEETGEFLPIQPAHQHISE TSGSANYSQVAHIPKSDALYFDDCMQLL AQTFPF\VDDNEVSSATFQSLVPWYSPG HIESPVFIA\TNQA\QSPETSVAQVAPV DLDMQQDIEQVWEEELSIPELQCLNIE \NDKLVTETMVPSPEAKLTEVDNYHF\Y SSIPSMEKEVGNC\PHFLNAFEDSFSK HPLHKNDPNQLTVNSLNSRM/PTVNTDF G*WNFILVF\MAEPSIRQAWPSPATLS HSL\ELLNGAHGCFDLFTL/CKAFNQ NHPEGTA\EFHGF\DSGISLNTSP\SA SP\EHS\VESSSYGDTLLGLSDSEVEEL DSAPG\SVKQNGS*NTMYSSSGDM\VQP LSPSQAEHFTCMDAQCEHTRGKDLPV \SPG\HRKNPISQDKHSSPLGGLISQR DEL\RAKAL\HIPIPCRKSFNLPVG/D FNEMMSKEQFNEAQL\ALIR\DIRREGV RNKS/AAASGICRKKENWENIVELEQDL DHLKDEK\EKLLK\EKGENDKSLH\LLK KQLSTLYL\EVFQHAYRDEGKPYSPSE YSLQOTRDGNVFLVPKSKKPDVKKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12618	26519	A	12743	6	457	RPRNRPGIRVDPRVRGRVGHAPHEGLVP ERMYRGSPTACETQAAA*ERAFGPSST C\RLPIPRMSTSVPPQHTWTQRVKKDDE EEDPLDQLISRSGCAASHFAVQECMAQH QDWRQCQPQVQAFKDCMSEQQARRQEEL QRRQEQAGAH
12619	26520	A	12745	297	12	QERPVRMLVLHFGRLRLADHLKLGVRDQ PGQYGETPSLLKIPKLSGM\MWAP*IC
12620	26521	A	12746	98	428	YNTSFNETVLLLTPTITIDCLYTRKDAI APESACGVCPCSLLGVGA*IPKVIRLD LSKKHVTAYGGFMCACVLDLRINRAFL IDEH\KIVPKV*KALSQSSKAFCEHET
12621	26522	A	12747	3	638	LWLWSLCVWVAVSLPLQFILGSLHPCQG QASWREVDLLHEGSQEASSKPSSGSVPV GLLLDQEMVTPLLVCICGILLHQEMVSP LLVYTRGILLHQEMVTPHPGLYPWDSPP LDGHSPPGLF\RGAAAPS*GG/PLPVLV YTRGAAPSGDS\PPPPGLYPWDT\PPS GDRHSPGLYPWDTPPSGDGHSPPALYP WDSPPSGDSHSPPGLFPRG
12622	26523	A	12748	2	333	DMVLLCHPGWSAGSI*KTKKERERMNL HR**IDRERERERERQIQ*KE*KRINEF EGSKERFTQSVKQRNK/ELEKIRLDT ETIYLSIYRN*SLRRGQERRTERERMH
12623	26524	A	12749	30	333	KTSYLLPVQWQAQNDNERYSSSKNTIMA LPLPLPVFPRSPSDAERKLDCSAISAH CNLPA\DSPASACRVPAIAGARRHA*LV FGFFWRRRFVAVMAGLVS
12624	26525	A	12750	231	39	INDLL/CLF*FKKLIWGRVW*LMPPIPA RWEAKAGGSFEPRSLKQ*AMITPMYSS MGGREQDPVS
12625	26526	A	12751	49	273	HLQVTEVFWFVVCVFFRRWGGSHCV/AQ AGV*WLFVTGTVPCCSPPELLGSRDPPAS AS*VAGTTGACLAANCRGF
12626	26527	A	12752	505	897	SYLRVQFYSAFSLFFRHEVLPCHTGWNA VV*SQLTTASN/CLGPSNLLKAPHLAN* KKIF*RQGLSMLPRLVLNSWPHMILLP* LPE*LGLQARATAPGSGFTFCLTQDSIL MCSPTVHKLSDSIALETQ
12627	26528	A	12753	335	542	CCNEFFLSQVWVWVMPVVPATR/SAEAGG LPGPGSQRRL*ARSKPVNSHCSAGRCG IDPISIKQKNNNR
12628	26529	A	12754	356	72	WHEYLLMEHTKKCHLS*GLYNGLNN*Q /WCTHPVVPATWEAKAGESLEPRSSRL* CTMITPANSCHCPAWATARSCLNQSIQ SSNNWQGMITGGK
12629	26530	A	12755	340	127	NYLFIYFRDSITMLPRLECSN*FTGSII VHITLKLGLSSLP/ASASQVAGTTGTRH HVQLSNYFKIKIKPKP
12630	26531	A	12756	290	511	KKNQPGT/CGSRL*SQRFGRRLQADHL\ DQLGQHGKAPSL/LKNTKISWALWRTPV FPSSQEAEMEELIEPTSSRLQ
12631	26532	A	12757	254	549	YPGAKKQRPBGDSVRGTHLQSRCWCVLL HNCQ*PKSNTQTFP*PKNLRE*NAT*KS TDL/WPGAAHLCPNSTLEG*GEWIT*G QEFETSLGNIIRPQIY
12632	26533	A	12758	617	451	NKKRRGLTLLSRLKCNVIAHCSLKYP GSSEPPTSAF*VAGITY\GT*HHAWAY

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12633	26534	A	12759	91	393	KWYTKCECLYLLVSIFSRVLLSIYREVLAQTLGKLSKTMCPALBETVAVNGLQIKSKK*/WLGVMTHACDPSTLGG*GGWIAWGREFGTSLASMAKPCLC
12634	26535	A	12760	10	221	QSHNTNGCLDLHFQKGPQSVGETLNL*TIPLCVCVCVCVCVRHVHM/CYIYSDFICPSIECEYFSAHR
12635	26536	A	12761	309	55	IIRYKNYISIKLEGWKRLYHATTHEKKVGVAVLISEKVDFAKN/MYQDKEGRFLL*R
12636	26537	A	12762	640	896	TIVLKCNEVLFCEFRDEVLCCPGWSAVA/QSQTQLW*TTQPGLKQSSCLSLSSWN*RHVPPHLMFLKTTFTLLYTCTGHLETNIC
12637	26538	A	12763	1	357	IVPLHSSLGDRVKPHLLKKKKTCTSLVIRETQIKITRYTYSNG*S*RKNKAGNNKCWHGYTATGTLIAD/CKSKQMLWKT*QPHIKLNIHY*YNSEIQFLGLYPRDKNIA RCGGLRL
12638	26539	A	12764	129	320	RWKCCKLKNTGQAWWLIPVIPALWKNQ\AEGSLEARSRLRQ*TLIAPLGYSPLPG*W SGTLSLNK
12639	26540	A	12765	617	435	GVKGLTLPKLQKLLKSTE/I/E*KLPKSFYDASLTMIPKLHKD\RPISHVKIEARILHKISINII
12640	26541	A	12766	243	5	QKIKKRIRKKNQNL*EIWDYVK*PNL*IGIPERGEKVNTENIFEGIIQ/ESVPL/AYLVREVDNQIQEIQTTPVRYTK
12641	26542	A	12767	101	16	RTQLFVSVFVFCFLFCFETGSCSITQVG VQWCHLRLSLQLPPPP\GSRDSPPPSSQN RG*TNI
12642	26543	A	12768	362	92	RVPHMDLGEECTSPYMYI*PMTCVFKHG *DGNFCVTYFATIIIIYTI/YLSVCVSI *I*CYLCVCVYIIYIIYIIYIIYIYKY MKERRL
12643	26544	A	12769	1161	824	QAKDLSTHFTKENM*MG/NKQMKRLSES LVISEMQIKTTMRSHLTHTRITIKMTS DKICP*RCG*MRA/LLQC*WKYKIVSPL WKIVWPFLKT\INMNISCNLMILFLGFY PIY
12644	26545	A	12770	241	237	K*RIWA\GVMAHACKPSTLAGCDGWIA*SQEFETNLSNTGRPCLYER
12645	26546	A	12771	326	6	DTVSRKNKSGKIFQLSSRV*IYERSQSG VKVYKCKTFGKFTQ/HF*AHMRMYTGE KPYKY*ECGKFFILVLLLLMIQKYFHL IKIVRLYLIRKKVSCQPSNKKILQS
12646	26547	A	12772	413	1	KKTFYFFFFETTQAGV**CDHNSPWP*P P\GSDNPLTSAS*MA/GLQSCMHHAQL S*FVFLEAGSHYVAQTDGDSPTSASQSA GITAVSHHTRPILYILIVLSYAISFFSI LYSAYFLQPHLPIHNNFLFSYISSC
12647	26548	A	12773	2	1055	FFFFLRLNLTLPLRLE/CVILAHCNLHF PG*SNPASASRVAETGSRHQARI IFV FLVEMGFHHVSQAGLE/SPDLK*SAHLG LPKC*DYRRDITPGHH*SF**RYFLKTY ISRVL/WCSLLGTFFMFIADFHM*TW*H *QNHFFHLLQIWKLISERLRSAGGQOAL KTVTSTFSSKYVCRAFLAEPGWIAILYV

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						TF*SLDSRRTCLVVAVSNFFYSTLFLKL RQQVLLTG/PYHLFSARPSSCGSDKKAR ELNLSLSL\CFFFFGKRVSQTQAGVQ*H DHSSLQLWPSRLKQCSHLSLLSSWDYRS ITPHLANF/CNFLSGWSRTPGLK
12648	26549	A	12774	315	98	FRCFNLNSINPLESPHVRKTCAGRAQWLA PVIPPFWEEA\SQMPQVIHSR*LEARS SRPAWPTWQKPCCLKYKN
12649	26550	A	12775	275	59	NPSPKYKIQKISAWWYMPVVLATR\RLQ *AEIAPLHSSVGDRAKPCPKQKTNKQ TKTSGEPLVQGPATVC
12650	26551	A	12776	73	381	SLNSELSSIPRPTWESPSTSDSAWPMQ NLASEPLPLP*TTPPDPFALSA/PE/P LPFTPSPRDTLPPPLSPSYKQAPVLSVH PFVMPKLYVSSPLLSSFLYL
12651	26552	A	12777	274	342	LNCVIA*WLMPTIISALWEAEVGVSA/P /RSLRPAWATW
12652	26553	A	12778	2	478	TIYYTKYTTFRVPLNLGLQLLTAFFCVCV CVSLNGFKNAKDYGGSHLKYSVYITGFL LQFSLKFDCFLCVCVCVFP*MA*KMPKI M/RGSHLKYSVYMT*FLF*FSLKLKYFC DFILRKRI/WPGAMAYTCNPSTLGG*GG QIT*AQEFETSLAKVVKPCLY
12653	26554	A	12779	680	453	SETDWRKNKFFPSNFPNLRNLTNSWTNSC SKKTFKKH/RVGLGVLATCNPSTLGG GGWSP*GQEFENSLTNMNVHFS
12654	26555	A	12780	59	487	SLHKKHPERGLQSFQGCWTQEMLGGSVQ QRAWELCAPNLTCPGYLSFFLRQDAL LSKLECSGTIPAHRNPSLSPQLKVSSH LSFPSSWNSRCTTPHQLLLFF*DRIRL FCPSWSAVAQSQPTVT/SSLPSQLKVS SHLSFPSSWNSRCTTPHQLLLFFNFL* RQVFTMLPRLVNS*VQAILPPWPKVL RLQA
12655	26556	A	12781	109	361	LSPWHHSRNYTLIYPYTLNFWMFAFPTP KEFFFFSFETRPHSVQAQAHW\AI IA HCGLDLLGS\SDPPTSAS*AAAGTTAII P G
12656	26557	A	12782	3	204	LIDGSLALSC*LFCGGATIAHCSLELLG LGQ\SPVSATRVAETTGVCCHHAQLAFVN LHLRTRSKHCGH
12657	26558	A	12783	2357	6366	LTGS\NSHTILTLLNI/NMGLNAPI*RH RL\ANWIKSQDPSVCCIQETHLT\CRDT HRLKIKGWRKIYPSPMGKQKKAGVAI\ LVSDKTDNFNPTKIKRDKEGHIIMVKGSI QQEELTILNIYAP\NTGAPRFIKQVLSD LQRDLDSTLI\MGD\FNTPLSTLDRST RQKVNKDTQELNSALHQADL\IDIYRTL HP\KSTEYTF\SAPHHTYSQNWTTIVG SKALLSKCKRTEIIT\NYLSD\HSA\IK LKLRIKNLTQNHSTT\WKLNNLLNDY\ WVHNEMKAEIKMFETNE/NKKTPTYQN FWDFAKAVCRGKFI\ALNAHKKQE\RS KIDTLTSQLKKTREAKSKQHSKARRQE ITKIRA\ELKEIETQKKTLQP\LKKISE SRSWFF\ERINKIS\RPLARLIKREK NQIDTIKNDKGI\TTDLTEIQTIREY YKHLA\NKLENLEGMDKFLDTYVSLPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LNQEEVESLNRP\ITG\SAIVAIINS\LPTKKSP\GPDGF\TAEF\YORYKEELVP\FLLKLFQLEKEGILPNSFYEASIIIPKPGRDTIKKENFRPISLMNIDAKILNKILAKRIQQHIKKLIHHDQVGFIPG\MQGWFNIRKSINVIOHINRAKDKNHMIISIDAEKGFDKIQQPFMLKTINKIGIDGT/YYFKIIRRAIYDKPTANIILNGQKLEAFPLKTGTRTGMPSLTSPLLFNIVFCPIVFWAR\AIRQEKEIKGIQLGKEEVKLSLFADDMIVDLENPIVSAQNLLKLISNFSKVSGYKINAQKSQAFLYTNNRQT/EEAKS*LMS ELMSEL PFTIASKRIKYLGIQLTRDVKDLFKENYKL\PLIKEIKED\TNKWKNIPTCLWVGRIS\IMKMAIL\PKVIYRFNAIPIKLPMTFFTELEK\TTLKFIWNQKRS\RIAKSILSQKNRAGGITLSDFKLYKATVTKTAWHWYQNSMVLVPKQRYIDQWNRT EPSEIIPHTYITILI\F\DKPLLEKNKQWGK\DSL\FIKW\CW\ENWLA\ICRKLNL\DEF\LTPYTKINSRWIKKKDLNVRPKT IKTEENLGITIQDIGVGKDFMSKTPKA\MATKAKIDKWDLIKLSFC/TICTAKE TTIRVNRQPTKWEKIFATYSSDKGLISR IYNELKQIYKKKKKTTPSKKWTK\DMNRHFSKE\DIYAA\KKHMKK\CSS\SLAIR EMQ\IKTT\MRYHLTPVRMAIIKK\SGN NRCWRGCGEIGTLLHCWWDCKLVQPLWKS LWRFLRDLELEIPVDVPIPLLGIVPED YESCCYKDTCTRMFIAALFTIAKTWNQPKCPTMIDWLKMMWHIYTMYYAAIKNDE FMSFVGTWMKLETIILSKLSQEOKTKPRI FSLIGGN
12658	26559	A	12784	787	926	PQAIRRPRPPKALG*HNSVDLGWAWWFT PAIPTLWDYTHEPLYLAKIS*CFKKVYKFVLNCIQNCPPHAAHRS/SGKTS*V*S NYLFFSFCEFKFCSVTQARLQWHDLNS LQPPPPGFKRFSCLSLPGGWDYRRLHTR SANFCIFSRNRVSPSWPGWSPTDLRRS AVLGLPKRWDRREPPCPAKIYTIMAPQ KVNHSQQPVVSFLS
12659	26560	A	12785	248	285	C*VIF*CVMIYVLIYVEKITSIRLAVY VV/CIIITRLFVK*ICSCLLGC*FLFFNV C*LYIFIIFVFFFFFFFFFFFFFFFFFELN ILY
12660	26561	A	12786	243	37	RRSAGHGGSCLS*SQYFGRPTRADHKVRS N/RGETLSLVKIQKVSQAWW*EPVVPAT RQAEAGADAWVDR
12661	26562	A	12787	75	289	DYRHEPRFFFLYTTFFEMDSHVARAGEH WCDLGSL*PST*GSSDSSASTSR\QRH HAWLIFGFL*RRGFAC
12662	26563	A	12788	83	256	RKMYVVGLEFVTAQN*K*PKYPSTEE/YI K/RLWYLHTMEYSSAIKIEKLGTARQNR LILY
12663	26564	A	12789	197	499	QSLKSVEETVFRNNKQ/SIPTFQVILMP WWLIPII*ATWEG*GRRSPLNPGV*DQP GQHSKTPSLQKKTFS*AWWRVPVPA\ IGAEVSGIPLSPERSRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12664	26565	A	12790	394	91	FYNSTKFKWKNIQFLITRCRGDQIQVIR AHAVQLGFHVLVYF/CLSQLNSIYLYISI YVYTYRYIHTHMCIIH*YLYIYTYIVI KH*KEHWWIKHCFPTERK
12665	26566	A	12791	735	75	FFFRQEGFLSPPKRGVPPPHTKKYFSP RGSFLWGWGTSRPPPRKCFSPPPPVFL PPPKKKKIISFSPTKLAPPPEYFKSPPP PS\PPPPSSPSPSTFFFFKNFPSPSSF SSPPFFFPSPAWEDPPVQSRRIY*FLPP PF*IPETPR\RVLKKKPGEGRSWGLFPP PKGPKRRVPLGPEFKTRLGHKTKPRFFK KKKKKKRFLISCLWWHMPAIPSTLGG
12666	26567	A	12792	482	342	MGVFVFFFTGSHSSVTWAGVQ*CNLSL LQP/PASSDPPTSDSRVAGST
12667	26568	A	12793	405	169	FYKKKKTGSGLALSRLCSCGTIIAHCN LELLGSRSLRL\SNTPTLAS*AARTVSV CHQTHLIF*FFVETGSCYVASA
12668	26569	A	12794	270	94	YVCYSYKQIKICSHVKRRE*NTFKIYLL KYIALGLTGHHFPL*TFSTVTLWPGAV AHACNLSPLEGQGRWII/R/QGEIKTIL ANM*IPVFLHVNIFLSVCSYSIHTLDY LFYYSYCYLISL
12669	26570	A	12795	284	415	NFIKIIKKKVMGLFYGKTFLNLKKKKR KKK*WPGTVPHA*NPST\LGGLGGWITR QGEFETSTLATN*NPTKSISRGF
12670	26571	A	12796	1387	32	APSSFAIRSFFSGPMNAFFSSMVWKRFP PNLEVVMNLRISIFSRARRFVCTSKDLR RVSTRFLVHLTAFLGYKAGMTHIVREVD RPGSKVNKKEVVEAVTIVETPPMVVGI VGIVETPRGLRTFKTVFAEHISDECKRR FYKNWHKSKKKAFTKYCKKWQDEGKKQ LEKDFSSMKKYCQVIRVIAHTQMRLLPL RQKKAHLMGDQVERGAPVPEKAD\WAPR EALSSKVLVTQVFWAGIK*SNFIGGDPR AKGYKGGQPVCWAHPRKLPPQRPHPRAL RKGGPVLGAW\HP\ARVA\FSVARRWGR KGLPFHRTINKKIYKIGQGYLIKDGKL IKNNASTDYDLSDKSINPLGGFVHYGEV TNDFVMLKGCVVGTCKRVLTLRKSLLVQ TKRRALEKIDLFIDTTSKFGHGRFQTM EEKKAFMGPLKKDRIAKEEGA
12671	26572	A	12797	86	364	EQDNRIFFSFLSLFFFFGETEFGPFAQG GGQGAILGLPKPPPRGL\SSPPT*GSQE VGTTGAPHDIFCFNKKGETPRLYKKNK NNRGGGATP
12672	26573	A	12798	101	440	HCSRYATGIFEWYSGILVLILLRFGIYE PMNLNIGDPYDSPSRLYKMRLWERMAL SLIEVSLKNSHFWLGMLAHACNPRTLGR IGGRIA*TWGF\KTSLGNIARPHLYLKK I
12673	26574	A	12799	364	195	NPPGDLGEETLLWGGEIMGTTPP*FPPP KEGFLPDPPGGFNSPPI/QGRSFSFPP PGKFGPPQGFFKRPPIFFFLLNNQ
12674	26575	A	12800	86	489	PTAMAEEDIAAGGVMDINAALQELLKTA LIHDGLAHGIRKATKALDKRQAHLCVLA SNGDETVYVKLVEALCAEHQINLIKVDD /NKKLGEVWGLCQIDREGKPRKVVGCSC IVVKDYGKESQAKHVIRENF*CKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12675	26576	A	12801	64	211	GNHKKSNYS LAPWYTTVPAT*EAEAGGSLE\L*CAMITPVNSHSLA
12676	26577	A	12802	300	3	NNVTTGSNIQFHSFPLIRKIDICVSYIKNDANNYIKNSNPNGETQVYQ*YSFSN*NLKIWLKVA\NPSTLGGHGGRIA*A*KPKTSMGNIVTPCLINKQK
12677	26578	A	12803	208	394	SQHFERPRREDCLS\QEGQYSEIPSVQKNVKISWAW*CMPAIPATREAEAGGPLEPRRSRL
12678	26579	A	12804	183	348	AFILGKGKYEYPYNPCLGWA*WCMPVVLA SWEAEAGG\SLEPRSSSEL*CAMLIGCLH
12679	26580	A	12805	397	238	ETEFPPCCPGWKWGDLSQQPLPPGFKR FSCFSLPSK\WGQ*SLAPVKGKCK
12680	26581	A	12806	1	293	PTRPRTSYEKQGYLLLPVFSIVLEVLARAI SQETELKSVQMGKEEVKLSL\FVCVYIYA*ENPVESTKTVDANLFDTRDWFHAI FPQTVGEVGMVLG
12681	26582	A	12807	297	281	AKNPRRQPREIPGGVFPTPGFPPYFKAKMPEGFPFGGFFFKGGVLWGTPPPFFFFF FFSETESRFVTR\LQCSGAISAHCKLRL PGSCHSPETC**R*G
12682	26583	A	12808	255	59	AGCSGSQLEFGRPRGV D H L S P G V * D Q S V Q HGEILSTKNTKISWVWWSVPVVG\EVGRSLEPGR*RLE
12683	26584	A	12809	247	310	PLHSILGTPTTPAPTGPGLLIRTSILY*KPILSQAWWCAPLVPAQ/EAEARGSL EPRDSRRS*AMIKPVNSHCTPSWALPRP LPQPLESHC
12684	26585	A	12810	101	477	IGKEEIKLLFPDNLMEYTVNF*MYKPLELIS*FSKVTEYQVNTK/SNCIYT*QL QIENEIAKTI*FMIASKSIKYLKISLTK CN\KWRDILCICIGRLSIIKVLVLPKLM CGGEKIFNPNTGFW
12685	26586	A	12811	1022	696	CFVFLFFKEMGSHYVAQAGVRWCDHGSL YPPTP\GSSDPPTSAS*VAGTIGAHHT WLIFKFFVETRSCFLIQAGLKLLASSYP SQPRTSPKCLGFTDVKSLHLAWLCP
12686	26587	A	12812	166	143	RKEERFQINNLFHFVEKLEKEEQI\NPK TNRKKKIKTRV*INEIYRKTIGK\IN KNKSWFF*KINKIDKPLAMLDGRRDSN Y*NITKSLIEGRRRKEEAGKRKEEGRKR RRRWRQRWR
12687	26588	A	12813	163	423	KAFWEFINHKKTGPF*RGPIGKVSPPGG NCLASSI*KG/DPFSPPLKGPQSGGPP PKKPPTGFNLAFGGLRGRETGRGPFFLAGLLP
12688	26589	A	12814	2521	2842	INTMYFPP*EMLVGWAWWF/RASNPQHF GRLRQADRLRSGVRDQSGQHGETPRLLK NTKISWAWWRAPVIPATWEAEAGESLEP GREGCSEPRSCHRTPVWVTRMRLY
12689	26590	A	12815	173	395	LDQPGQQRETLSLLKKKQTNKQTKKKNG FKKFL*LDTWVHTY\NPTPLGGRGGGFF *GQDFETLANMGKRGFY
12690	26591	A	12816	43	346	CVYVS/GVCVCVCVCVCLASVCMYVCLH L*VLFGIFYV*DHNI CKLRSCFLFKNT FSHVYF*KIWPVEL*VTVFLFLSSLL HTSCVYEKSYAILIFSAL
12691	26592	A	12817	647	931	SQHFCRPRADHLRSGVQDQPGHHGETP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLLKI\QKLAGRGGGA*L*SQLLGRLLKQE NRLNPGIRSCSEPGSHHCTPAWATE*DS VLKKKIGADKY
12692	26593	A	12819	392	2	PLFFFFFFFLETESHVSQTQAGVHNPPGP SKPPTSAP*AAATTGMHSAHAQ/LIFF L*TELPSCREPGCSAMAVHRHDPFTDQHG SASFLIWASSPLLRTGDSSLLGGHHVD AKFSVDTQLALCTKAQNS
12693	26594	A	12820	1183	870	DRVSLTLPRLGVAVARNLAQWKPLPPGF KRFSCSLSPSSWDYKHTPTPG*FH/RG *FFVFLVETGFRHASQ\AGLNSLPQSDP PTLA/FPKCW\DYR\HDHLAWPRKM
12694	26595	A	12821	172	298	IYLSIYLP/ILCIHLSIHPSIYPLYL SINPSYWVSFSREL*LT*L*YLSIYLP IYVSIYLSIHPSIHISYPLIHPIGLF LENFD
12695	26596	A	12822	51	254	YDFLKKHLLSSYRAKDLESFLHLHLHF SGN*SVSYICVCVCVCVCICVCVYICIL IKSWCS*S/CGVL*AICAGVGWC*LIFG VL
12696	26597	A	12823	199	668	QPLPAPSPSAQKGRAHPTSPARPQAE/ SLPSQSLGTRTRPPLGRPP*SPPWGQVD LWGWLGPSPTLPAPESLSPASLSTEVVL CGTRYLVWGRSGAGQA
12697	26598	A	12824	33	442	GRGKLLKKSQKQRKNALLKYDSKTRVGT LEHWTSPVTRPPLL*INIRLIKLDVIK CSIHKIFHSEFLFFKQHSGL/CI*LSK* LCS*KIHQSGLGTVAHVCNPSALGGQDR RIT*GQEFETN*VNMVGPCLYPPLPP
12698	26599	A	12826	363	75	HWEPRPAGPTLPAPGSESGRCPDHHT SG/PPPPNTHTPMSRSPSWEGSDQRPO PBHTDTGSPEN*GSRLRHERPPWGRERQ RPPPTTLVRPLSH
12699	26600	A	12827	76	486	CTVNLFIYFEMESCSVVQTVGVQWCDLSS LQPLIWFSCVPTQISS*IPMCCGRDLVE GP*MMGAINSFLLCCSYDSK*VS/ARSDL FFFFFFF
12700	26601	A	12828	345	672	KMKCTADLSLLEKDT*IKLEENR*QERI MLRAEVNEIENKIENKTTGGSSSEKYY- KIDNPLTRSIRRKVN\KITSIRNEKGSV TTNPTEIKRTVKEYIMKNFMPINLT
12701	26602	A	12829	208	1	PSNSTPIFKRNENICPHKDPCTLMMLAA LFVMSKK*KQLKCSSNDE\KLWYIHMME *YIAIKRNKLLI
12702	26603	A	12830	649	172	FPLKYSLSSTSVMAPSFTSCGGSQQVLL APLSRLAWPNV/HPPPQPRHPAPHSFL SPPRSPPNYSP*SSQGPLLQPQSKHVRP LPQANARLPSAKNPARGPPGAAQAPRDR PPA/VCPLPPHSPLRHERAPRLFLPLP ATEPAALHAVHPGRRQERV
12703	26604	A	12831	1068	667	KLSWFFCSRLRLHFGSIFKVPSP/LPVPK LLLPIPSLCPSLPLQLQPAQVPFNTAT WLCFC*/P*RV*PAPGYQVRVGHFNFFPL QLNFIPILQ*HLGF*KSASLSSSSSPK KVSLLCHPGCSAVVRSACNLKLLIS*SA CLGLPKC*DYRLQSPRPP/PTIFKVTM CLLKSLTGVSF
12704	26605	A	12832	268	1	KCFFLLALNWPEFILDYFILNW*NSLRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VTEKFLEMTLFLTY*NMNRPGMVAHACNP PS/TLGSGSGRIT*AQES*TSLGNIVIP CLYQKL
12705	26606	A	12833	654	321	LVGIRFLKVKYFNIKFPHELLATISPSLE VFNLQHFIYIFLLFIYF*ETRSCSV\R LECSGVIIHVCSLKLLGSSNPPALASQV AGTTTAHHCAQQHFCCILEKSNLCITYFPL
12706	26607	A	12834	867	201	RQMSPTRLTKSRDVASRSSFSAWAWGKL FTWFDFMSLSVLQGPGGFPHSQP* TQGR*VENNQEPLATPFPGPERSLPGQPRL EPAHSGKKRRGLPLEIRPPVNVSDIHGDP SGAQWLVRGVEAGPWAVGGQAP*SEGPS PSPPLDVSPPDGSSLPRSSSP*MDLRA* LSLTF*TFQKGSGN/DPASSPA\GKPG* EWRIKIGPPPQGLLLGPPEMWGSQARVLS
12707	26608	A	12835	328	1365	YAFCLMMLDKKQI*\AVFLFEFKMVHKA AKTTQNISNTFGPGGTANKHTVQWWLKKF CKEESLEDEERDMGHGKVDNDPI*EP\Y *TT*KITEELSVDYSTVIRVVQHSKQIG KVKKLDKWVPHELSGNQNYRFEV*SSF MRNNPNPFLNRIVTCNEK*ILYN/RPAQW LGPRGQLQSQFPKPENLAPKKKRSLVHW/ SPVGLLAPILDPTYSFLNP/GGETITSE KLCSGKLGKMHGKLYLLPALVNRKGP \LLHDNT/RDCVFAQPVQLKELG\YK VLPHPYPSPDLSPSYHFC*HLDNFLQG KH/SQHGAENAFQEIVKS*STDFYATGI NK/LFSHWQKCVCNCGSCFD
12708	26609	A	12836	7	328	RRERERERERERERERERERERERERER ERERERERERERERERERERERERERER ERERERERERERERERERERARV*EKST RYKSPPPRIPLLR/RRV*RKHPHARAL SFFLYKKCTGGERAPSVCVGGKFTW
12709	26610	A	12837	219	350	PFNHTYATWSIIISNVQVCFMRAQDIYL LIYLFEAGSCSV\RLCESDMIMLHC SLDLPGSNNPPISAT*I
12710	26611	A	12838	189	359	LGLDGMRVGPCRALGPS*EEKSSRVQW LTPVIPA/LLEAEAGSGPEVRSRLRP AWPTW
12711	26612	A	12839	368	77	KNPNFLKFGSKPMGPPIYSPP\LEG*AG GFINPGF*TPGYMGKPPFLKYSNLPG LAAPGGCSPFPGGLGRKISFTPMEVSI NPGSPLSLPPGEQN
12712	26613	A	12840	16	173	KTDVHSKTCTRLFTAALFLIVKKWKHLK PP*VD/EINKMWNHIVEYYLAIKS
12713	26614	A	12841	425	45	NSFVFFFFFLFNRLVLTVPAPRL\CTGV IL/APHCTLPALPEFKRFLVPSALLSSW DYRFPVMPWLNFCIFVETGFH\HVAQS VLKLVSLKL/PSPTWDVPC*DFRYSVR CCGLFF
12714	26615	A	12842	237	375	LLLTVVYILKKLW\LGVVAHACNPSTLG GQGQWIL*GREFETSQVM
12715	26616	A	12843	21	325	TSFFFLESYSVAQAG\QCWDPGSLQPQ PG/SQ/DNPPTS*G*VAVTTG/MHHARL IFVFFCRDGILLYCPRSKIIFSSCIRE LFKKISDFLLTMLIFCNSNKG
12716	26617	A	12844	369	58	PISPLOFMLPFLKNQSPYGPFFFWKKKNF PPPLGGAVLKTGPF*NLFKKIORGF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PFPKKKKPRERPKPCPPKFG/SPPPFFYPGFPPPKKGPPPPPPPPPPFF
12717	26618	A	12845	211	409	NALKPKIHFFFSGGGLKGIWVGNTLLDIGLHKTFFF*GDFYYAL*I*AENALFGGGDCAPHLQVK
12718	26619	A	12846	200	33	QKTNTKWCQGWGATGTLIHF*GEFTRVQSHWKIVWKFL*/SLNILP/SSSSSSSSSSSSSSSVKNLCLHKACTWMFIAALLLAKTWKQP*CE
12719	26620	A	12847	416	125	KIPTRPGKGGPPLYPRPFRGLNKQIGLTPEFGTPLGNKGKSFPPFQKNKN\NWPRGGPIGPPSPGG*VGGLTLKGEVSTKLDSPAPPFGGQKWPLP
12720	26621	A	12848	85	397	KIHIFFFIFLVSLKGLSFLLTFSKN*VF/SFIDFLILCVCVCIEFYCFILILFHYFCLFGFCLFLMFVS*QQLDFYFNSF/YIF*YKIQCYKF/CILIF
12721	26622	A	12849	1	246	RPRRHLVASLVLTLQNLGSSPLPIKIISWAWWLMVPVPTFWAEVGGLEPRSSRQ**AMI\SPCPPAWAT
12722	26623	A	12850	161	1	NKTTSSQIW*PMPIVSTT*EAEVGGSLRPRS/L/KLKCAMISPVNSHCTPTWTTK
12723	26624	A	12851	65	244	STYYLHSLPFLDISYKWNHTTC\SRFIMGALFLIAIK*KQPKRPSADEQI*T/IMWYIYTLEYDLAIKRNEILHAATWMNLKNIMLSKRSQTQKT\HVV*FHL
12724	26625	A	12852	235	34	TTIAVSVLILKELMEP*TLQPDFLG/WSLITESVDHVQWHAPVIPALWEGEVEGLLEPRSLRPAWATW
12725	26626	A	12853	168	453	CQLRGASGTQGGFLSESQCQQPCP/PECRPSKPRPCGCRI*SPARTSPQSPASMAALPTNERTPPPAKW*PK/CPKQSPQSAKSKSPVKSTERTAK
12726	26627	A	12854	244	3	ELQVYMHIT*YI/C*SIYTKANIYIKYMHMCVYIYTHTHVCIHLHIYLLRHGFGCWLMLGKVRGCEGMAGLMKAQQCWGW
12727	26628	A	12855	376	428	KWEPGGHTSFFFFKGLVLNFGRGVLQKTRP*GGGQGGKFNPNFSGPREPPPP/PPPGGGKKGPPPPPGVFVFLEKGGSPILPRGVLNPGAPKGVYTQRGGIKSGNQGATPLSFFLKVWF
12728	26629	A	12856	129	395	APPNTHPFLSEAPQSLSLRPPSPAPSNSSSR/PPVWRASQTHPPQDWSSHCSPPWGAPPQI*PFSDSLAHPQDWSSHCSPPWGAPPQI*PFSDSLAHPQDWSSHCSPPWGAPPQI
12729	26630	A	12857	363	97	GLATLRLVSNLSQAQVIRPPQPPEVLSLPKC*DYRPGRPASLIHVNSRQT*KVAP/CSKPLAAAAHQSGPATETTRCPSRCGPPIF
12730	26631	A	12858	322	361	KSEKQS*VMLAVCTLDMMKMT\FISVVF LPKTHN/LMSNYKKNTRQIPMEGHSTIYLTRIPQNCQGHQKQ*KSEKQSQQESKKK
12731	26632	A	12859	88	417	HFTFFFFFFFFFFKRCGGFFSPRLKRLGKNFFFLDPPPPG*RDSPSPFKEGGF*KP/SPPPLVFFFFFF*KKKGFPAGAGGF*TSGPGETPPLYSPEVWFFYGGTGPPTPFFF
12732	26633	A	12860	217	2	LILINKLANMHCFLEFVFETSLT*AGVQW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HDL/GLLLRLAPPRFKQFFCLILPSSWD YRCALLHPATREDEA
12733	26634	A	12861	375	145	LSFFFFFF*KPGSCSVAQAGVQWHAHSSL QLQTP\GFSDSLNSAFSVARPVVHCHT RPLSPFNICWRARPKQKVFL
12734	26635	A	12862	525	852	NLLSIYFFETESRSVAQAGVQWCHLGS LQPLPPRF*IKKPSNTALEF*NLLSIYFF ETESRSVA\RLCSGAILAHCNLCPLGS SDSPASTSRVAGVHHHSHLSSWDYSCAP PCLANFFVFF*VETGFHYVSQDGL/DTS *PQVICPSRPPKVLGLQA
12735	26636	A	12863	3093	204	EPDKTGPVLWKVGGGARVPGMAETLSGL GDSGAAGAAALSSASSETGTRRLSLRV IDLRAELRKRNVDSGNSVLMERLKKKA IEDEGGNPDEIEITSEGNKTSKRSSKG RKPEEFGVEDNGLENSGDGQEDVETSL ENLQDIDIMDISVLDEAID\NGSVADC VEDD\ADNLQESLSDSREL\EGEMKE \LPEQLQ\EHAIEDKETINNLDTSSEDF TILQEIEEPSLEP\ENEKILDIL\GET* RSEPVN*ESSELEQPFQDTSSVGPDRK LAEEEDLFDSAHP\EEGDL\DLASEST\ AHAQSSKADSLAVVKREPAEQPGDGER TDCEPVGLEPAVEQS/SVAASELAEASS EELAEAPTEAPSPEARDSKEDGRKDFD A\CNEVPPAPKESSTSEGAD\QKMSSPE DDSDTKRLSKEEKGRSSCG\RKFLGLVG LSSTTRATDLK\NLFRQIWGRVGGAPRL WTNARSPGSAFVYGFVTMSTAEATKCI NHLHKTLEHGKMISVEKAKNEPVVKTS \PKRGSDGKKEKSSNSDRSTNLKR\DDK CDRTDDAKRCDDESVEKSK\DKNDQK\P GPSERSRATKSRKSRGPKRTVV\MDKSK \GVPVISVKTSGSKERA\SKSQ\DR\KS ASREKRSVVSFDKVKEPRKSRDS\ESHS RVSERSEREQR\MQA\QWEREERERLEI ARERLAF\QORLERE\RMERERLERER MHVEHERREQERI\HRE\REELRRQOE LRYEQERRPAVRRPYDLDRRDDAYWPEA \KRAALDERYHSDFNQERFHDHFRDR GRYPDHSV\DRREGSRSMG/SIREGQH YLERH\SDPEPH\QDQSLR*LGWGYEL* Q*RLS\EGRGLPSFPPGAGRDWGDWLE DEDDPVMGKGTAERGPMMDR\DHK\RWQ \GGERMSGHSGPGHMMNRGGMSSGRGSF APGGASRGHPIPHGGMQGGFGGQSRGSR PSDARFTRRY
12736	26637	A	12864	2	456	IHLGSGSEGDSGGLGRGNSNTSRFSS SSWARGDNVPRPPPAVCSWISEGDVQN PGLGEAGAGSSTPGDGGELRY/WPGLLG A*GRGIGGDDDDLRTLGLAGVQCGKG/ RRGPRGPGRGQEPRRPRDLGLRGPRAQ GAA/SATAAPPP
12737	26638	A	12865	388	1	LIKMTKVKKTAITKC*RGWGRTGAFIHC SWECKMIQPLWQTVWQLLKKLNLYL\WK QPKCPLM/VKWIKKLYISMDSYSAVKKK ETLMTYTA*MTLEVALLSERSQTRKGER GHILWDSIYINFQKMQTNL

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12738	26639	A	12866	198	3	KKQKQTKNPPKIS*ALWCVPVVPATWGA KVEGSPE\PRRSRLQ*AMITPLHSSLCN RVTRGRTRG
12739	26640	A	12867	415	973	NEVNCAQFSLLPTEYMGHRVEGATGHG TCPSVPPNTHLHTGWCLQHHRSRAWG RGGSHTHRCQQRVPDGEHP*YIYIAVHGE PP/ESPPQPSPLSCPPQGNIALREPP QGLPLPGTLP SHPPPFWHICKTHSSES HPPFPFGFCGLELEKGVDFIHPPLTLP KLPNPLKPEPTPTPQTHI
12740	26641	A	12869	715	893	PCVAPHSTIREERFRLTSESTNQKVLWWG ID*T/VILILTGNWQKRHLKSFFLGQKP GGMAP
12741	26642	A	12870	342	58	KKKKPKENEQSIWDMWDFNRTSDI*TTG VLEEQFRE*GRKIIFKETVRENSNLTK /QINLLTQEV*TTT/HKNMNKSTPIHII IKLMKTTTKEKI
12742	26643	A	12871	110	401	SFYSVMILKASRIVICLET*LYAYIHTL YIYTLCTIYYAYVNIYICTHI\NIHII HVYTYIYIYASIIYYSMAWYNIKVS KDRQTYENIALITYY
12743	26644	A	12872	439	256	SYFMRFGGDKISKLYQFILSRRWKQSTC PSMDEWINKMWH/ITIMEYYSAK*RNEY SYMRHE
12744	26645	A	12873	356	43	GTPERHSHSHSQSGSPIIGAFMGIRASV YSLSCVLLMLSPQRVLEFYFSAFKQQS \WSGKVAQAYNSNTYGKAGSIT*GQEFK TILGNIARPCFYKKKFLANS
12745	26646	A	12874	341	205	REIKKMVLNKKFFSLQFLGKKKNFWEFF LKKKKKVKFAPPVFQF*VPIF/CSF*KK KVFGFFFSPIKIFFFFFFFFETESTSV TQEFNGTILAHCNLGLQSSSSPASAF* VAVSQDCAIELLGDRGLCLEKKKKKKK KNFSGKKKSKNLFLLKRRKMG
12746	26647	A	12875	474	206	PIRANGPVFSPPPPPAPGTCPHPLVIM LSRHLRQSHPTTVQPWTSGLLPSPPA* LSLETQHFKTAHFIFP*H*SSGLGPGWG SPVGEPPG/HPKLCQPAAAAEAWPPRE GTKARRHEGLPPAPCAWGPAPRDAGSRL EFPTLPTIPVSQSPGR*HGAGGRPSCLR AFVPSRGGQASAAAAGCRQSFGLDALLP LGSPILGQQNFSARGR
12747	26648	A	12876	257	467	YRVFTLLPRLEYIMAHCNLDLGSSDP/P QVAGTTLK*LSRASRVAGTTGVHHHSWL IFK/YFL*RRWRRFSL
12748	26649	A	12877	867	1409	GPTVLVGGQDWN SVLQOPRAHSFTPRGG AGGLGGGYVLHKPIPFSSQELLGAFPCQK QYRVPPPLEAQLLRQARSPAFIY*AAVL CQAQGPSPSPCSPMVSPRPSGRAPHGA APQSGQKALASTSSDAEPV/SVG*WCP SNPALQGGQNGAEPRAVSITSGALSLYD CFLDGWWEGRSLGP
12749	26650	A	12878	1416	740	IRNPRWVQLDVFAAAPMGRSSPLFLLLF SFLKTVLRGSMIPSTVPS/FHKGPAACL YSLSLRS*SQAAPSPAPSSSLTPSPHPG LTQPGRGRRKADIS/CSHSAFYVP/SL PHLPWACPLSLPQPVLFSLFCFVLF*D GVLLCHPG\WSAMARSWAHCNLHLPGF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QFSCSLPSSW\DYRCMP\GLG*FLEF *VEDGGFTILVRLIWN*PQVIHLPP KVLGLQA
12750	26651	A	12879	961	31	PSPVRDSCVAVAGERRGLGGSGVWRSH ARGPGLMRGLPASEPAPCVLGSRPCFRV AFETPWTSPASCMFERCPLWRPPALVAA GLDPFLLSSTLTAVCPDLIRSWKKGC DVCDNRNCWSTHSPACRDAILAPILAG RGEICGLWG/AAAAGTGRV/TPVSGLTF STVDFDSSARG/V*GGLPRSTGGPRVRG PGQPVPLPGLPAGVALAPLEGRPQEPAP ALSHSLTGSFLGAWLCGCTRHGRAPVL LEVSIACGQLCEAAPQIFIQPGLQLP TPSATSPAYLWVDVLLTLPVVIKQKRV SFLTKE
12751	26652	A	12880	232	28	PALWVPVVARFDGMEETGQNHWSKEKAW PGAVAHTCNPNTLGG*GGH/MT*GQFEF TSLANMAKPRIPP
12752	26653	A	12881	331	1	KNGPFFKNPEFFPPPKWGVPPNPPTVF PWPEPIF*LTPGPLKKQKIPFQ\KGEIL GWGGKMGNLPFWKGGPPRESKSSPRF YKTPPPIFKKKKGGSSRSRTSPRV
12753	26654	A	12882	370	287	VSILAGCCGVAMIDNTVLVHKEVKILRK *IIKK*CI**FRGHSK/HNFSG*AWWLM PVIQHFRPR*GSLEARSLRPATWQD PHLYEK
12754	26655	A	12883	656	1168	EPSRGVWPHEHDARINGSKKKKSKDKRK REDEETQLD/IVGIW*TVTNFGEISGTI AIEVDEGTYIHALNGLFTLGAPHK/ER IALKPGYGKYLINSDELVV/GRSDAIG PREQWEPVFQNEVRNGGPAEMGEKRN GTKWREDTDHTSFPLFPSTGGQPKAHNS WRKVCH
12755	26656	A	12884	205	452	ASGSAHRFRFTSFETGRVLDKPSQTDHT NRKRGPPNVK*SFL/WLGAAAHACNPNT LGGGRRTA*AQEFRTSLGNTVRPCLY
12756	26657	A	12885	112	290	KYNIIQYNIVFSCHDPLVSFNLFPPPPF GKGGFPLSPRLKARGRVGYLNPPLPGK RNFWAPPQGFEEKGLPPP*SPPFGGVG QAKNLGPGFQPPAPMGKTPFF*KNQNN PNWGGQPLNFKTLGGGGPKISF/PPGGG GLNNPKPSPGPSTWGKGNPLSQKKKK KD
12757	26658	A	12886	406	190	TRSLARGGFGRPLQKPYWNEQSFTMAKK \YEQPKCPWTDKWNKMWSILTVG*YAA MKRRDVLTCATITCR
12758	26659	A	12887	440	160	RVCVCVCVCVCVGVFCFALWLSLTIYN *VYLFLFVHNLGRVSFSYFLNLI*FFE VNHV/HNYVQMIQNTKLYLKSYLETFH/ CPC*FPPILLH
12759	26660	A	12888	201	411	HIWDVILIRHALGNFLTISCIYIKIWL DAVAHTCNPNTLGGQGG/WIT*SQEFKI ILGNIGDPLSTKKNK
12760	26661	A	12889	138	464	SCTMNPSEMQRKAPPWRWRHS*APSTH KMNRMVMSEQMKLPSTKKAEPPTWAQLK KLTELA/TKKKSLENTRGTTQTSKNMLFA ALMIVSTGCAGVPSSSKETATIEDKP
12761	26662	A	12890	146	366	FSVSMKYFV*IH*FYHL/KLLLMVYL*Y

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GFLAINTSQNISCSQKIMKLHL*GRGVV AHACNPGTLGG*GEWMA*AQEFNTGLSN TAKPYLDF
12762	26663	A	12891	368	50	KGRQSGVSSFPVGTVTNLTVAHNRY LFPHPGCGQTSEVKVLA\GCSLLKASRG EGFFPLPGSGGSKCPLAYGCITPISASS CDLLWVCFSSYLAY*DTCHWI
12763	26664	A	12892	227	456	KLTTLLKLF EK\IEDRTLKSKSFYEVST *IPSSSSSSSSP/ISLNTDAKKINKIP RNRIQQCIKKIIFHKFSTGIYS
12764	26665	A	12893	461	89	IYQNLSRKPDNIKCW*RCTEIQTLIHC W*QCKIMQLLWKI IWQFL*/ELNTEVPY DSIPLLDY/PKKTEC/YTSTQTLLIYCM NPIEYSAIKRDKVLIHATTWMNLENI/ ISKRRQSKSTYCMIPLI
12765	26666	A	12894	222	185	RIVMQYLHLNLGACVCVCVFVCD/CVCL CV*MCVHIHIYISTHTYIHIYVCM*ICR LS**CEFYS
12766	26667	A	12895	186	166	IFFFFFEMGSHSVTQARVQWHNHSSKQH PPP\GASDPPTSAY*VAKINIFFFF
12767	26668	A	12896	55	485	TCWDCRDEPPRPALESVFLTSFLEDEFS IEIADLVPHPTPCSHPIQPP**VIYFC S\KPLVTGSSSPPRKPPPSLHEPKSASL *PPSSTIQPVRSSPKG*PSPPLA*VQFP KGMTIPTLCLSPVLPVPSTIPLPNVSKP LFFY
12768	26669	A	12897	923	312	VDVIRKVQIEITLRCHLIHVRIAIKKT RANKCW*GCGEAGALVHC*WEC/NYILV QPLWKT VWRFLSKLKI ELPYDPAIPLLG ISPKGNEII/CCTPKFIAAQFTIVKIQT QPRCSSMGKWKI KL/W/HIERSIDR*LE YLAFAKKKAVLSFAKTWIDLEDIMLNEI SQTQKEKYCVISLICIGIKKKKVYIEIE NKTIVITKVRIRWRK
12769	26670	A	12898	320	3	ESWRWGRIVRPHSVPGETWLCVPVPPGPP NAPDGSFPLAICPVPPSCRSI/CP/DD CLASAGV*GGFPLPRTEASPHHSWACPQ EQPWPPQCKLKVGA PNSTALSEGS
12770	26671	A	12899	138	447	IFVFHYKTQNIYNEDTLHVIIINLWCYP GSYIKSTGRLRPEVERGLGPTTMC*FS SIKNIFYF*KLKSYRKL/WLGTVAHAYN PSTLGG*GRWIT*GQKFNRD
12771	26672	A	12900	279	1	INQSIHNNIKSTYISQCKLIQP*WKI IW RFIR/NLKI ELLYVPATPPVGV*LKELK SAC*RDNCTT/M/FTAALFCIGYGSNLG NSTALIGSRVLFPP
12772	26673	A	12901	235	183	IINYGGGPPEKKKKGGKKIPLIFYKKIK KFLWPKKKKLFGGAKNPV*AHHIFTV* IDVDTRADFTSATI\IIAIPGVKVFS* LATLHGSMNK*SAAVL*ALGFI
12773	26674	A	12902	180	19	LFIYLFYLFICEIRCHFVTQAGLQW\L IIASC SFALLGSSDPPTSAS*VKGI
12774	26675	A	12903	406	949	APVPGHGFVCSF/CGENGVS LYCPGRS* TPGLKLC SCL\CLPESWDYR/R*APVPG \LGFVPHLTL*KPPFFKDYMKSLFQFLK YLIQG*CTLV*GVRYS SFIFFFFLRR SLA/SVTQAGVQWRDLGSLQSPPPGFTF FSRLSLLSSWDYRRPPPCANFAFVFLV

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						EMGF\TVLTRMVWIS*PCDPPASASQSA GITGVSHRARPKFVLYFKDNGEPLGGVL HRSHIAVHWM
12775	26676	A	12904	265	385	GNGSPSLRWIGVLRGRSPTELELRH*PIF LTAASRRSLDRVSVPMWGTFLLSEPLSIE GLVSRYLTTNNLMERIPILYRN/PFNNET M/PESLCYRVLIIFLSKGYPRVKGRDLTC YSPVRRSPAKKASFLPDAPRLACVKPVA SVHPEPGSNRTRG
12776	26677	A	12905	363	137	APGMQA*WCM/HCIPGAQAEAEAGWTEP RSSRLWCTVIMPSSHCTPAWATW
12777	26678	A	12906	315	565	TPVDHGWLECSGAIMAHCSLKFLGSRDP PASASRVAGTTGVCHHSQILFLFFVGT SNFVAQAGIELLG*\VILLPQSPKVLGL
12778	26679	A	12907	376	412	DAWPTWRNL*FGVYVMTDR*EPRQMLTY LTA\PLKYFKSGVMAHSCN\ PSTLGGQG RWIT*GQEFET\LANMEKPCLY
12779	26680	A	12908	215	2	NIHINGQKLEF/WLGVAHTYNISTLGG RGGKIS*TOEFETSLANTVRPHLHKQK IALPLPLPLPLPTVR
12780	26681	A	12909	307	379	KR*KQPQYPLTEEWINKMRHV\LQYYSI LKKKEIL
12781	26682	A	12910	279	123	KMILSWARWLMSIIPAAWEAEAGGSVEL RS*\LRLE*AMTVPLRHFTPAWARE
12782	26683	A	12911	1	194	AKQHIIPLLARLECI/GLFTNTVTAHCSL ELLASSHPPASAS*VARMTECVHRAWLE WIFYLCVIL
12783	26684	A	12912	206	388	IELSKQGPVYKQWYVITPPYFPFFFFFF ETGSCSVT\RLCS/GTITAHCSLNLDP LSYSPTAAS*VAW
12784	26685	A	12913	238	426	TPLLPSQQWLKESLWLGRVVHACNPST LKG*GGRDS\RGQ*FETSLGNIARPLI REKFLKI
12785	26686	A	12914	115	1436	AKDRHFTEV*IANKQMKRCSTSLGMRM QSKIVRYHLSE*/R*LFFFNCGNCWQG/ CKK/IQDLIHCWECKMVQPLWNIW\RF L*NHTCICHASGIALLSIYPREMKTCVH TKTCIRMFIAALFVMVETWRQPIYPSLG G
12786	26687	A	12915	282	21	IKFPPCPSTWGTTKKLFFPKKKKEVMKML CFHFNLLVQNI*YRLGNEISDKAG\PV AHAWNPSNLGS*GELIT*GQEFDTSLAT IVKL
12787	26688	A	12916	254	150	TLPGRSSDFSLPEV/YLKNNH/WLGVV AHSCNPSTLGGKGGWIT*GPPHMLKVSF LPTDPTSRVKQLYNWVPHSTVLIALFT KNPG
12788	26689	A	12917	181	24	AQWCDGIPVSKGNL/WLGMVAHACNLST LGGPGRWIT*GQEFETSLANEFHRTD
12789	26690	A	12918	75	298	LFILFTS*VD*MRPTHKENNL/LAQST NPNVHLIQ/KHPRHSQNRVWPNVWAPH G\QSSCHIKMTIMARPSGSQL
12790	26691	A	12919	251	9	KFMFLARCGGSR*SQLSGRPRRADHLR PGVQNPQGHSQYLPKSTNFCRVWWC TPVVPATREAEA\GESTEPGRQLQ
12791	26692	A	12920	198	211	RFCFVSGDEREGKRA/RERNRETERKKQ TEDTETQREERDRDRK\ERETDTERER PREERHTEREKK*KAAFFPQTLGCRAQD

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12792	26693	A	12921	438	127	FFPKQLFPPSRGWGVGPMTVLL RVVMERIFVRPHIKDSMWWVRSTLLGRG DALNDLFLYCWEKEDPRYKERP\RE ERERERERDRCEWK*APGWRERPVQSLR ACHPPWHRFALAGPVPSAQ
12793	26694	A	12922	158	460	EARVELLLSSRCCKPRAVITAETQPAVYR LQLEIENFPGLSPRLECSGAIHAHCSLD LLG*SDPPNSASR\AGTTGMCHAQIVNS CKADWLVLSSRGLTHR
12794	26695	A	12923	33	484	GIQAACIPGLRLSPADAHCHRHTPSPP PSSTAPRDDVGPMQITPDNFPQDPPL\ TPPSQSLLPHRAP*PQGSSVDLPGLLFK LPQMPQTPGPEEVDTCVQIHKTSKARED VQMRKTPMAREGRHRAHRWIGALGKAP QSQRRLRHTVG
12795	26696	A	12924	335	332	RIKVYVRGHAK*LRPGP/VAHTCNCHT LGGQGMRI TQAQEFETSLGDIRPHLYK KKKKKGGPF
12796	26697	A	12925	302	407	AQWLMAITPAPWEAEAGLLEPRS*\AW VTW
12797	26698	A	12926	766	244	RVPRLLPPPAL*LEFSPSGRLRLARSHSFQ LRSSPPPVSPST/PFSPHRSPPLSLLS LSVPS/PPLHHSFFSQRAHILPPPLI FPSSPPAPPPPPSSSSPSSSSPPPP /PPINWGTPRFFPPPPFKNPPPEINFGG PKKKKIFSPRA*KFVFLKGPPPPFFFF FFFFLGINLL
12798	26699	A	12927	127	720	WCGLLESTELQLQSLPLGYVSVIFGKIF YISGLGICCTKIFPSALPSAQAASLPL PARSALGIVFFLHFC*IE/CNYKKLP HHI*LIKTFSYGLT*LFFFFFFKTKSLIF SPRLNCRGPFVLN*NLCLRG*GNSPA*P FGGAGIEGAPHKAGLIFGGGGGAFLKKT G\LHHVAPGGASNSGTGNISHPPLNPPK GAGE
12799	26700	A	12928	308	49	KEHW*AVGHFNICVTGGP*GERKKGTER VFKEIITPNFPNLIQTIKPKTQETQHTP SRRTKI/TPRYIIKFLKTSNKEKILT TAR
12800	26701	A	12929	375	2	GCMLSLKTINILEVLANVLAQKKIKRRK LND\EQADTTFTI*FCVRQTKKSTDKL VKLI/ERFYKVATYMINFLKKSNSFHTP ATINC*KQIPFIMATKTIKYLRINPRKK CVRFGKKLTFPER
12801	26702	A	12930	202	379	SSENFSGKTVNLCCLGRLHRMISWLHTV AHACNPIT\GWIT*QGEFETSLADMVKP CLY
12802	26703	A	12931	209	376	TVGEKMYLKVKRI\WLGVAHASNPNTL GGQGGWIT*QGEFETSLGNMAKPHLYKK
12803	26704	A	12932	280	31	ISCKVTKKVTLFELKYIWNKFYIYERVS IVGTTEAACEVTSNVITGPGAHAHACN PST/RGRWIT*GRELKTSPANIAKPRLY
12804	26705	A	12933	1	189	QMYTESEP*CKLWTLGDYVNM*FIS*/ IQCTTQAGNVNIRE/RLCMCSGGEYMRN LCAFLSILL
12805	26706	A	12934	108	409	HHSHLLKLPNVWFSFCHFIVTVFLSL*R VFFVFY*IFLSSSHFLFSFCFCPIFMIM FPFKFILSCNIVFI*NIIFFLF/VHV*G

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						*STLVSLFVFFFLQF
12806	26707	A	12935	225	11	ILLCMEPSFLFWFGFICFVKTGSHYIAQ VEVLWLFSGMIKVHCSL/KLLHSSNPPT SAS*VAGNTGSSYCTW
12807	26708	A	12936	74	12	GTHASAGVINILVFILSVFFLTHSLCI HISKYMFVYICVCICTRDFYTEFKSFC TFCFFGSSFFLEKKFPLVAGLEQGGK LG*LKPPPPRLKKFSCLTLP/ABE*RT NG
12808	26709	A	12937	166	311	PHS*WECQMVRAPELENWQFLTQFIRGL PL\DAALPLHM/CHRKCTQLFIALLI VAKKCNHHKNL*ANEWINKM*YIHTTDY PLAIKQNEILIHATTWNNVVT
12809	26710	A	12938	51	296	LCMYTLHTLYMHTCIYAYICYTCKYIHR Y/LHT*IPEDANSVKHKYTHTHIVHTL VYPHTTYLMCSYIYSWVCVCVCYIYT
12810	26711	A	12939	426	28	KGFNLVNPVFPSPRF*TPAPVFYFCGP IKKIFFFKAGGVKFDLSKRAPLFFFLK TGSCFVP\RVECNIGIIAHCNLCPRSN DPPPSDLQVTGVKPPP\AKLFFFLW*M GFHHILDYQGETCLSQLLGR
12811	26712	A	12940	11	213	ATAPGLFSFFETGFCSVDQAGVQ*HDHG SLQP*PP\GSSDPPALASQSARITGVSH CKGPEHTSLLT
12812	26713	A	12941	416	38	WLNNHSRLGFPNCWDYICKLPRLGPDVA SLLIHNSS\GTWYGATKLESNWYFSIPI YKDHQK*FAFTWQQQYTFVTLPQDYVS SAL*HNTVHRDLHDLDNPQNTLVHYS DTMLDLMSRKYQAL
12813	26714	A	12942	361	74	IIHPSFSVSSRNHKNAYPAALGGYSVY GVAILLFHYFINKLAFTLHCGLA/LNSF LR*IQEPPLG\SGSGPFCNVFLAPTEG TIVQKPDPMATFG
12814	26715	A	12943	125	401	SSFEPGRGIPLNPEVAMQKESVNILCSPR SQEFLESRIKIKVLTDLTQDEL*GQAQ* LTPPIPS\IWEAKAGGFLEPRSLRLRSC HCTPAWVTE
12815	26716	A	12944	92	306	KRTTNSPWGCSAY/GVAILLFL*IL/KL LAFTLLHGLPSNSFLRKIQEPSLG\SGS GPIFGNKLVAFGGLMIVVS
12816	26717	A	12945	322	24	NFKKNINLNPFLRGYFLFLKGGGLTFK KVGEPLKKKKKLNQQFSYFLSTYTVK* NN*/WLGAVARTYNPSTLGGRGGWIT*G QEFGTSLANMVKKILAK
12817	26718	A	12946	2	448	GGAPMKRHGSLDRNYRVDTTRPSQLFLF QLYHNYLKFAYEATKEYMHRKETLCLPC PAIQFSFPKSNLCYRGYLCMRTCAHTQM *MYRYITYVYMHYICM/YRAICTYTYT FE*KYILQKCILLCIFLFFLQYLYVSY LNRHHFLIAA
12818	26719	A	12947	155	415	LLETGGNAGCSSWMHVLLGKIHRYGMGS RPISLMAG*\GPPWLRVAGLRGRPATL GLRYGPDYSYGRQQW\EYCTMGASLMQRR RVRD
12819	26720	A	12948	247	250	KYVYKYIHIVYKCVYIFTHVYGYTYLYT DVYKYTYLYTDV*ICICIYKCIYLYWYI YIHLGINMYIYIHLGINMYIHIHV*YIYI HIYI\HVIYFIYIYFLYTVYK*IHIEVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EYIYTLWLKL
12820	26721	A	12949	25	407	EALSLLLLLVLWGLLLGIARKMYQQMNL VQYCLLVLP*P*NL*EQKRFEREVLGDLHR EP*FHVLCCTHSEKSFRRFSW*EL*IRK LTLVA\GGVAHTYNPNTLGHRRIT*G QEFETSLGNVVRPLFL
12821	26722	A	12950	370	106	ILYLETLKSFISIRSFSAVDSHFEEKS TVGKMLPNSITCTDPI\FNKKKSQMLWQ SSLPPFSQKLPQSPQPVSPSPSRQGS IPATR*QLA*GSVQVMLFGSILPTVELF SKWESTAEKLLILINDFSKVSRYKIYV
12822	26723	A	12951	280	319	DQPGQHGTFL*VSH*KKKKGWM/PGVY AYNPRFLGGRGGWIT*GQGFETSLANMG KPCFY
12823	26724	A	12952	337	113	TQLAISLLGICPRDLNLTVTCS\SDTCTQ MFLSVLLMVAKR*KQPKYLQIDEWINKM QCIHMESYLVSKGRKYLCKL
12824	26725	A	12953	9	186	DPTVCCQLQDTHFTYKDTNKLKVMGWTKY /CHANGNQKRAGVVIQIEYP*SKSLKSE IVQN
12825	26726	A	12954	46	381	NENTYSYKNTQMFIAALFVVTPNWKQP TCPS/SGEWINKLL\YHLMVYSAVKTN /ILVYVATSVNLRILILGKQPDKKRVLT V*PHLYRKYKLISDRKQIHGRLEVENK GK
12826	26727	A	12955	19	250	CSDMVLKACIKKLMYSYKMGHIQAMDYY TAL/NKEL/LMYATI*ANLEDIMLSKIR QTQKDNCLMVDCIYIRYAEQSSL
12827	26728	A	12956	173	163	GAKHSASGTGWIRKDFTRPGAVAHACNP STLGG*GGWLSRSEFETSLTNMVKL/CL YKSICCTRCLLGCFFPQALSKAID
12828	26729	A	12957	301	79	EKDNQPLLTNRNVLHAIKESENHRIT ELKVTLRPAVAHTCNPSTLGRSG/WI A*GQFEFISLAKKVKPCLY
12829	26730	A	12958	314	126	KHHHFKKHNFRLCVCVCVCVCYKHF YLFSLSFSQ*P/CICC*CVCCSFLCCF *SATYLKII
12830	26731	A	12959	529	1697	VPFMGHISNFFFSPFLRQKYLALLPRLG VQWQ*SRAHCNLRFPQ\SSNSHASASRV AGITGACHHGWLFLVFLVETWPHHVQ\Q AGLKT*PQV\SACFSLPKCCDRRCEPL CPATSSILNL*TMDRL/PGEPKNQ*NLL VSFMCVAFYREGQQHVYFQRLWCKREF IVRSPWAINLEKGGRLMGAV*IRIMLNL TLT*GFCTEDEKTVNSRVNQKLTPT*LG DE*DVKREKNINDEIKLLTCNSRYTKSY RLGR*IKLGAFCFPM\VPMGQTGRNGQL KVQV*TGTVAHVCNPSTLGG*DRRITRV QEFETNLGDHSESSLQKIKLARHGAAR L*SLSL*VSWDYRCSPWP\SNFCIFK\ RDGVSPYWPKA/WS*TPDLQSAHFSPL KVLG
12831	26732	A	12960	1	395	GTREFRILSEKFKKEIDFFFFFKQSSP PPGPKKQTL/C*KQTTPTKPKQKTNLGP KFGGQPKPKPKISHPQIGPPKKKNYP* GQPVWNPPGEKKEGPTPKPKDPKANLK VMGLKGGVKKRGGKTFPQRA
12832	26733	A	12961	90	436	LWRLTSPKSAGWAGNLETQESMLQFKS

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						EGHR/PAESPLA*SSVLFSLSTDWMRPIL/MEGDLLYSKPIHFNVKISSKNTYRN IWNVWPHV*TL*PSQSD/CLK*TITPILVLLTCTH
12833	26734	A	12962	415	463	LRAKDQVLPKILVC*TLFFCAQIKKKK K/WPGAVAHAYNPSTLEGGGWIT*GQE FKTS LGNMVKPSGIPPHWI
12834	26735	A	12963	774	316	SISPTCSGKIGGKLNHRHFSKEDKTG\RY MNKCFISLVISECYLPK*EDTH*TP\LR MAKIKRADH/DKC*QRYKMTGTLIQC*R ERKMVQPLWKT*QFLKRLNIHLPPDSI PLLG\IY*RKMKACVHTNTI IWMPIASL LVKAK\AKQPKCPSTR
12835	26736	A	12964	44	395	MYFTLVWGSIGPKFLGGHQPLQGQGPFL HFLKAL**FFFPQTPGNGGGTTPAKTFP PFPTPLSSSSPCPSPAEGGSREPSLSTP /SCLHLYIGGAASNPPSPPLPPPQCSG LGYPVC
12836	26737	A	12965	424	50	MAFPFLSCAPDAINNNNKKCCRETNNEE PPNEPLKWRHIMIFFFEASHSFAR\LE CSDAISAHCKLCLPGSRHSPASAYRCPP RHLANFSAFLVQTGPPRVSQDGKDLQTS *SALLMPPLDPAIP
12837	26738	A	12966	245	44	QSKELGNYPLPSPSPSPSPAFHGLPPP SSPSPAFHGLPLLP\SWTVQPQ*RLTAT SLEDPASPSPRG
12838	26739	A	12967	205	30	QEGASLSRIKRGPGVGAWLGMVAHACNP STLGGQG/SWIT*AQEFETSLGNPHLYQ KYKN
12839	26740	A	12968	114	465	DEVSNPETTKPEPPPKKTES*P/EPKSL LWLPS\P*NSS*CANREQPPSPQPHLP HPLPTSLQVHRLP**SLPPNLFPTLYD /SPEPSLLPVIQFPA*TSPP*PPVYSSP PSPTCPLH
12840	26741	A	12969	1618	1038	VHMVQDKDINLNNQFLSGTMLLFFKETS HR*DRGPGDF*SCLYSAPIPTQPLLF*Y LPQNFIEG*PS*NSRIKGTSLKTYISRV PSFFFSFL*DGVS\TVQAGVQWHDLGS LQPPPPGFKRFSCLSLSSWDYRHPFLC PANFLDF**RRGFTMLARLVNS*PCDL PASASQIAGITRMSHHTLPHVFP LNV
12841	26742	A	12970	197	411	EQALRSTVCYCLNPLPPAPLRPRQDC\G PCRFRWMPGGRTRWLAPVIPTL*BAEAQ VWLEARSLRQAWATW
12842	26743	A	12971	616	777	MGIHGVRHNAQLNFFVVEDGGEWQLTC TGAGDSSWVLGEP*VFAC/PKNVLFYLH P*LFG*I*YQLKITF*NYEGMVP/FVF RFLFETRSLSPQLECSGTITTHCSLEL VGSINSSISAS*LDGNT\GVRHNAQLNF VFFVEDGGEWQLTCTGAGDSSWVLGEPL RYYKERLIKWYL
12843	26744	A	12972	222	389	VITEALGSDELEGRQLWW*IKIHSQVQW LIPVIPAL/LEAKAGGLLEAKTSRPAWE T
12844	26745	A	12973	425	145	QIIFFLFQKIKNQFNKASFFKKMTLEQM TSRQKNSAQISVFKKNSKWITDLNVTH *TIQLTGKN\NIGKNLQDQGLGKEILNL TLKAQSTKG

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12845	26746	A	12974	322	411	NNKKIFMSTS*KFFYCFIVQLIFETILS VRVLESIIILINYL*YCIICIFPFLFL*T *EIRKVTKFTSFPOIEEK*KCRR/WLGT VAHTYNPSTLGG*GGRIA*AHEFETSLG NTGRLPSVQKIL
12846	26747	A	12975	428	1	SRKSSSQFRLSFFPSHFLDLGAKGAVSQ DRAIALQPPGPRSR*S*RPPSRPRCFRR PRPSRSRSNKERAGEKRRPRRSLQPRPP HIAGP/VPRRQGSPSAGEAPLATDEPP PQRRSGIRGGSANIRSKQTSSLRPRVRG RVG
12847	26748	A	12976	60	294	NHCTETVLFQ*LTCVCVCVCVCVCVCT ERI/CFFKFLIGKGTGCIYLWPKTFIL IFIYILYSRGRSILKKKFFFLT
12848	26749	A	12977	6	341	DSLTLPLGLECSGAISACSLCLSG/FK QFSCFSLPSSWGFTG/VPPRMPQLIFPY FSVKTGFH\HVG*AGLKLILPPASAPK CWDYRREPPRPDGLWNF*PTGFKLRFPQ FPL
12849	26750	A	12978	296	42	SQFASLGFKSVLDLPLLAFCPLGKITLTL WDFSFIYYIKQE*WPRAGIFMPY\NPST LGGRGGRIS*AQEFKTSLGNIIVKPHYL VK
12850	26751	A	12979	20	373	KLYGGIWGFFFFRRGLNSATQAEMQGHN LG*LKSPPPG*RNFPASASGEPGTTGS HHKAGIVFYIKKKPGLKTFTLGKPTPPP SFRHHQPAFPMGVYSEILGEKSLTNGWD PQTKKG
12851	26752	A	12980	380	96	PVFPPPWRAQKGSIGREIRPPRGNQK PGPP*KKKKNYPGGGGPPSPFPPEG* PKKWHNPGGGTTP*TEFPPWPSTRGGEK KPPSKKKKKEK
12852	26753	A	12981	331	71	ELLIYSWVWCTPVVPATW*GRELVGRI T\KSRRLRLQ*AKIVPLESSLGDRVRPC PPPTTKKLANLCPWTEGSLSFSYLLEQ FHSC
12853	26754	A	12982	383	189	RRALKSCAHSTPAGPKNAALSQAQWLTP VIPTL*EAEAGGSLELRSPRL*AMIEP \CTPAWVTE
12854	26755	A	12983	144	6	ILAQ*KTWLSVVAHTL*S/TLGGQDGR TGAQEFKTSLGNTRRPCLYK
12855	26756	A	12984	341	509	ETLYTME*YTAIEKNEIMSFAGTWLELE A\VIL\SNLV*EQKTKMLPCSPLMGWEL K
12856	26757	A	12985	387	125	DLPTTPPKLEPRTCSVAQVEVWCL/GSL QPQPPGP\SDPPA*AS*IGTTGTRHHA *EMFPF*VYFVQTSEHILGINPPGRHTK VAWEV
12857	26758	A	12986	151	350	GRGGF*PLP*IFPPGQERPGFTPPKAPP PLGFFFP/RRFFFLRRSLALSPRKWRD LGPLQPPPPPTPGY
12858	26759	A	12987	251	1	RMSLLEKRRSNN*EARV/CGRVIYVATE VIKIMIGISMVAHAYNPSTLGGQGRRIA SAQEFETSLGNMTNPCLYKKYTHKKSRA
12859	26760	A	12988	320	3	TPWGVKDFSPPPPPGEGVFPPGRAPPR* KFFGNFWKKRGFPNWWVRGVLFKFWG\KNF FPPNLPKSLGLRFKPPGPP*KAPPPFPL FFFFFEMEFLCCPGWSAVAQS

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12860	26761	A	12989	353	183	EYGTHTLTAAIFSI AKRWahr*GSLTDE WVRKNSSLQSM EYY\SAIKKNEVLLHAA P
12861	26762	A	12990	377	2	LSIILINFRFSLQRGKYPGPPPKKNP PQKTPPRAPKKKKPFFFFFFSFKKNF PFFFKGQSKGGFGPP*PLIFRFK\NPP PPPQKIGFKAWVFSTPPPIWGF FFF FLRWSLALLPRLEC
12862	26763	A	12991	134	298	PPNSYCDGSITLIPKSDKNITRKEKYL/ P/IYLMTIDAKVFKNVLPNRIQQ*IKRI I
12863	26764	A	12992	892	171	QT*SH/SLSRLEYSDTIIAHCSLKL MGS SDPPASASQVAKPTGHCTTMPQPHTEGF
12864	26765	A	12993	269	2	GLWCFVKQLKLTETCPHFVAVPQFPLGIS KIPISILFFKKLLL/WPGTVAHTCNPST LGGRGGWTT*QGEFGLMFHHWPSKFHHG QHGET
12865	26766	A	12994	324	4	SLYPLLFQAEIYFLVTIHRSSMESCIYF FSVVPLDSLVIQIHVKI/HIKIGIML*V N*QNCFKINISE*L*YIWPSTVADTLGC QGEITRAQGFKTSLSNMTKPHLY
12866	26767	A	12995	106	531	WLLNLFAFLNDKGFVPMNRSRIFSQQK VKQRSFEGCSSFNVDGSCYVTQAGEQWL FTGVIGTL*PGTPG\SSDPPASASQAAG TTGS*HHIQLNLILYSSG*QTI*LL*TT DSTHLIFASLYAKEQLITFYFQATSLQP CT
12867	26768	A	12996	1	367	NTEPFLNIFFKDKVS/CSTIAQGQWRL YSRCSLKLGGSSNSPTSASLVAGSKGRH HYTRL*LFFYVSRPQDYLWSPVFFFSF FLSFFFWKGSFFLPPSWKARAPIWVNGS LPPRVKPIFLA
12868	26769	A	12997	3	379	YRPSSETKAVLVFFSFFSFFFLGTPGG KGPPKGAPNPTLTWRGKENFFI*KKKKP /RLI*KKGPPPKMGFKRERFWVLKPKGP QFGKGEKG/SPNYPHPRGDPKAPSLWKK PQFPGGGGGGAPKKAS
12869	26770	A	12998	230	409	SCRPKLLAFLKSSTEISQRWKQPIYI/ PSTDE*INKMWHIHTMEYYSALKRTKVL IHATT
12870	26771	A	12999	310	343	DPVCTII*ICDIINL*IECSKVW*SLKF YKILILFNVCVWPSVGNCHKWLCDCVV* KQW/LWPGMVAHTCNPSTVRGGGRIV* GQEFETSLGNIVRPSLYNNKSCI
12871	26772	A	13000	390	289	IKLCQPRGVKLDSPFKRAPPPFFFPETRS CFVS*AGVQWCN/LGSLQPQTS GPNPNTSA*LSLIFMCSNSYVCIVK
12872	26773	A	13001	1	289	GILRQISVNYLPVGRSLAQAGVQRCDLG SL*PLPPKVKQFSCVAGTTRGCHHAWLI FIFSRG\GHPVKGASSDSPTFGFSKAG ITRLSPRALACT
12873	26774	A	13002	359	105	KQKKNPSPPPGGGGQGGKPG/PPKPF PN SRDFPPKNQSPFFPKLKKKFFNFY*KAK NP*KPNPPLKKGKPKGFFSPPPPLKKP PNV
12874	26775	A	13003	243	293	MNSQFLKRL\RIESPYGSVISLLGTYST EK*KACPCKTCTQMFTSALYIIAKKW\N KCPSTVRW/IKLWHINTMEFFCQ*KKFH

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						CIDMPQFVHLTVEGHLSPFCYYI
12875	26776	A	13004	465	307	SEACFILKLFMFCG*CCLFVC\SILLVF YFVFCFVLCFAAYMQFFNQCLFG
12876	26777	A	13005	207	3	DGSLTMLPKLEC/RWLF TGVIMAHCHLE /RLGSNDPPASASRVAGTTGVCHHA*LI FIFFVKMRSHYPTRP
12877	26778	A	13006	2	56	DLALLFRL*CNGMITAHCNLK/RPG*LL GSRDPPTMVS*STGITGMSHEAHRPSPS CDF*RSCSVVQAVVQVHWDYSSL
12878	26779	A	13007	402	74	FGASLLKRHFLFFLSKPLVYNKKIPRPL VFLKKT\PPPPGRATPFYCCFFHKEGP GFGVKKEG*PKG/SPPPPQRGSTPPFFL GAFKKPKVTTFFFKKNPKTLKGPPFF
12879	26780	A	13008	356	145	RPPPPFFFFFETVSHPVAHAGVQVHDS LQL*TP\SSREPPASAS*VAGTTGVHYL PGSQLPILEHSPPR
12880	26781	A	13009	227	353	GWSELT*/SN*AQWLTVPILAL*EAEAG GSSEPRSLRSAWATW
12881	26782	A	13010	249	32	NPDShSWAWWCASVVPQTQKARVGGSL SRSLRLR*AMIVP\CTPAWVAQEPLSLK KPPTIETLFSPQDPSQ
12882	26783	A	13011	247	403	TPGGGGKYFFFWGPPQKKNRGGGFKNGGG GKTRGPP*KQPASSSPFAPPPFFWGAPG FSPPPRF\KPPPPVFFLGPPKKKIFPPP PGGLFFFLLGGPPSPFFFFFLLGGGPL FFPGLGAMGPMAGFRSLAPPGNSLSKKK KSEGLGEGGNSVLTRVLLISSYQIPGNP R
12883	26784	A	13012	206	386	TREAQTFWFPLYS*KAL/WLGTVAHT*N PSTLGGQRRITSSQSESETSLANMVKPH LLEI
12884	26785	A	13013	354	31	YKMNIWDIHI*HT\YIPVVPKGKERKR KKLEEYL/QDIMTKNLFNLMKNMNIYFQ EVQQTPSRINSQTSTPRHIIKLSKYKT GREQWILSVMLALWEAEVVGPPPEVRS
12885	26786	A	13014	1	419	EETSFGKARCLPGYPGFHRRRLRSRPL LS*MPLSHPPQGPSQPPAGSMSSSPATT STCSCSPPAAGCTRGRTTGRPFWTASGP AELD WASGSSV/EALTSGLPARGLWGQY AGLGVPRLGLPMTSCCMSLPFPSPARP
12886	26787	A	13015	109	426	TSLGNIARPH*QTHMATIRSVPPPSWKD ST*LRHPPPPHMC/PD*SLKSN*Y*H YLVNP\IWPMLTLLFVCLFVCFDRVSL CCPGWSAVVPSRLTAASLWVQVILPP\ RLAN*IFFLRWGLAMLRLV*NSWAGDI LPP*PPKVLGLQA
12887	26788	A	13016	149	422	LKRIFFLKVVFTHDTAPGDNDMCPYSC F*NQIIKSGLFFFKPHL/WLGE GAYPC NPTLLGGQGRIT*QBFETTPANMAKP LLYKKYKN
12888	26789	A	13018	162	377	QSPGYPERVSKLPTITQRGMWMMHQP CTSL*NV*TGWAQWLTVPVPAF*ED\AL AGGLLEVKNLRPAWST
12889	26790	A	13019	205	427	IQTGGPPARPFLWPWAPGKK*RVPP PPKKKKKTTPPHPGGEREGS/PFSKKKK KKTPKKRAGVFFPGGPRPKEGPGWGP LDKFPVGAPEPGRGLNGPGKIFFGPGP FFPLQPQKGRP*PGGEGGSFFFLLGVPP

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12890	26791	A	13020	248	358	LGEPSIFCLDLPENA SRCGGEAQWLLPV/I/PAF*EAEAGGSF EPKSLRPAAWAT
12891	26792	A	13021	2	434	ITEAGSDTQEIHTHTLYTHLCVYWRFFTK KAQVKKKVVWHM*PQLLRLEMGGSLP RSLRLQGAMTLPVTSTT\QAWAT
12892	26793	A	13022	162	410	LTQKTAASQIILSFSSTSLKIPISSES GGGGSVSVTQAAEQWRYHSLLOP*TPGD KRSSHLLGIPHP\SSWDYRISKDWVMPV
12893	26794	A	13023	250	40	LIKLNIFSCSLAIWTSSCMSTSLFKYFAH FSFF*IDFYSSYYILDTPNPFRRN/GITN ILSSSVTCSFILFVV
12894	26795	A	13025	264	1	VSSTKHGKRLLEPEY*CFIHH*EEKVFE SYFEY/PCQTFILRKETVRGAVAYACNP STLGGQCRWII*EQEFETSLTCIAAALR VTLR
12895	26796	A	13026	110	523	CIDSSSWTQTDRCEDRLCPGTTGTGTCAP GLLFLSAPPLGPF*PSQAHPSFHVSLSG PSPGLRPQLDIPHPSTSIAPRPLPGPA S\LPRLPEHPSLPSPGTGACPFLLPCLGE QRHWPLPTSLWLGLDGHCLATPSVS
12896	26797	A	13027	52	53	CPTLLQLTLC/LPPQASAMVDAPP*ARP LPPSSILACCTSGEQGSVVVGLAEPVKG YNLLVCRLLRPLEKCGIWWAVSRFSLYS LSWLPLARKG\NPLTACASWVR
12897	26798	A	13028	262	381	HFGRRLRQVDRLSPGVRDSLCKNVKP*QI IYTF*FSVSLSVINTYLGKPSVTAHTYN PSTSGG*GKWIA*AQEF/TSLECNKVKP CLY
12898	26799	A	13030	1	846	FRPIQAGRPAWALTLP CMGFTGEGSPALL SHSSRCDIQMGCNTHAVDDSTGEGPFHK GRMRESCWLRTPRCGLYTKGVGGPGMEG RERRSRRRQHMPGRGHSTMASWSLRQC MRLKLQWASDILLSQLEMQIPSLPPGESG SLGLTGPRSLH/CEQTIGLSPTPGESWS EELG\GGIVGGGRGTVAGRGHREAGNK PSGTWGRQCCASGDKAMSI*LTSLY\AR RGEPPGPRPVRKWLRESSQNRI GGEGR WE*GQRRSREGRECPVGWGRKKPLRWG LMWS
12899	26800	A	13032	308	1	KHYHDFWCWIIILALSDAQSLDHTCV\CV CVCVCVCVCVLRDQGSLSCL*CEG*LVP HFVPGPVLCLLSPVIYVCFICSLTCKVE SLSNFFKKLNKALLRHCI
12900	26801	A	13033	763	244	FLGPRIIGLRHEISVETQDHKS AVRGNN THDNYENVEAGPPKAKGKTDKELYENTG QSNFEEHIYGNETSSDYNFQKPRPSEV PQDEDIYILPDSY*L/CQNIDFCYWMIN IHCNFS TAKTRNQT KC*STVDWIKM WY TYTIEYYAAVKK/DTKLTWEQIKYHIF SLKSGS
12901	26802	A	13034	326	58	EHYKCNVCQKIFQKL*/HL*SKKHVYAE DKYYKYKDGVVPLLSQIILYTFYTRGK P*SSCSNFVQNQIIYIGQKSCCKNKF GN TFFKKP
12902	26803	A	13035	199	3	RFIYNHVKCITTFPLPHFYF*KLVL/WLG TVAHAWNTSTLGG*GGRIT*GQEL ETGL DNTARPHLHTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12903	26804	A	13036	94	448	GSCATSMAPKFDTRKTAVEPGVVHGI R I KPLEKVCADLITGKKFKNL/KVKGVP CM PTKTLKITTRKTPCGESSKA\WDGFQMR IQK*LTNLHSPSKIIVKQIISISGAPGID SEVTNADG
12904	26805	A	13038	964	1717	HKLSCVKDLKDFMRQAGE\VTFA\DAHR PK\LNEGVEFASYGDLKNAIEKLSGK\ EINGKNINLIKGSK\RPSRSRSRSDPG TQKSP LGPRSRSPSPVVRKP*QPVQEAR SREPGARSQVPVPVK*GPPPCPEKEPQK \RGS LQSKILSPPSILWIRPEVSGPRSK VERSVDSGN
12905	26806	A	13039	2	725	SLLFSPVLPFLFLPLAYILQNLKPLQF SPDLKSKHLIFFCNAA*PQYKLDRSSK* PENGTLNFSILQDLNNSCRKIGKWSEVP EVQAFF\SHQSLPSLCAQCNS/CPNLPS FPP\VPVSVPTPSVTESE*SSFSTDPSD LSLPPQALLLARPS*VPILPQPPLLHPI ILLSPPLLTPRPAYSFIP*L/CPPPPAQ QFTLKKVAGAKGIVKVNAPFSLSQIR*H LGSFSSNIKIQPSSWLWVQQP
12906	26807	A	13040	1131	2	DGVSLSPRLECSGTISAHCNLHLLCLN DSPASAS*VAGITGPATTPPLIFVYFFF LVETGFHHVQSGLELPTD\SDEPPASD SQSVRITGVSH/AYLACSQF/CTRC*FP II*EQCVNMNINSSK*IFILISYLRWM NKDPI/VIIERLLVRMPEGQSHAAN*NK TNKQT*ILELVLVTSCGVSVRFNLSIP *VFPSTK*EGWMRCVNPSTLT*FIQVA *TCQEHGLMKIQ*NPGLDPSIVSDHQT Q*EPSVKQVLDISHDKLMSLEELYHCR HTLASGKQISGVPRITIFLNHFHGFYFIY /CIFEMESCSV/SQAG/VQWRDLSSLQA RS/PGSR/RFSCLS/LPVQHPPPGPANF \CIFSGDGVSPC*PGWSQSPDLVIR
12907	26808	A	13041	97	626	ICFTQVKVLNESQVQWCMPPVVPATWEAG AGGVLEPGS*EL*/CPVNSHCPPAWAT
12908	26809	A	13042	2	431	HDPDTHSQIKVIKLMQSEFCWGWAW*LT PVIPALWEAE/AGGSPEVRSS
12909	26810	A	13043	405	1319	RYRKKLQNKPLWLH/CLLLLPSNATR*T LQK*SK*ISPLESSA**KEPPFLSVLSV TSVKT/SAIPMPPHWENVNTQVPYQLIP LHNQTHEYNEVANLFGKTMDRNRRIKRIQ RIQNLDLWEFFCRKKAQLKKRGVPQIN EQMLFHGTSSEFVEAICIHNFDRINGI HGA VFGKGT YFARDAAYSSRFCKDDIKH GNTFQIHGVSLQQRHLFR TYKSMFLARV LIGDYINGDSKYMRPPSKDGSYVNL YDS CVDDTWNPKIFVVFDANQIYPEYLIDFH *FHFQISVVKEALFFFAGRFALQSSSH
12910	26811	A	13044	23	450	RSRAAAIQLGQRLRLPGPDSPLRTGRQL EPGTGRGSRAGRGPCSIFFRFRRETTPQR EGGEALGATSRQAPPPCPPRPQWELDAS AKAAAVAPPKVGFKAVSRDPRAEALGG KGSP\GGKGS LKGV AHR*GGLGPL*GAP EAI
12911	26812	A	13045	172	16	AHVSPEVDKTKFW/LGPVAHICNSSTLG GRGGQIT/R/QQEFETNLNMEKPHLY

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12912	26813	A	13046	181	9	YKWGPAMLPRLKCRAT\IGSNMAHCRLLD LPSSSDPPSSASQVAGTTGTCHLGARGG MV
12913	26814	A	13048	2	3507	YVRVSLPPPPPAAGRPGA AVADDAREEE EEAAPPPPPPPPRLLAARPPGSQPRPP AAGEAQAAADMNHQQQQQKAGEQQLS EPEDMEMEAGDTDDPPRITQNPVINGNV ALSDGHNTAEEDMEDDTSWRSEATFQFT VERFSRLSESLSPPCFVRNLFPWKIMVM PRFYPDRPHQK\SVGFFLQ\CNAESDST SWSCHAQAVLKI INYRDDKSFSSRI SH LFFHKENDWGF SNFMAWSEVTDPEKGFI DDDKVTFEV FVQADAPHGVAWDSKKHTG YVGLKNQGATCYMNSLLQTLFFTNQLRK AVYMPTEGDDSSKSVPLALQRVFYELQ HSDKPVGTKKLTKSFGWETLDSFMQHDV QELCRVLLDNVENKMKGTCEGTIPKLF RGKMVS YIQCKEVDYRSRRREDYDIQL SIKGGKNIFESFVDYVAVEQLDGDNKYD AGEHGLQEAEGVKFLTLPPVLHLQLMR FMYDPQTDQNI KINDRFEFPQLPLDEF LQKTDPKDPANYILHAVLVHSGDNHGGH YVYVLNPKGDGKWKCFDDDVVSRTKEE AIEHNYGGHDDLSVRHCTNAYMLVYIR ESKLSEVLQAVTDHDI PQQLVERLQEEK RIEAQKRKERQEAHLYMQVQIVAEDQFC GHQGNM YDEEKV KYTVFKVLKNSSLAE FVQSLSQTMGFPQDQIRLWPMQARSNGT KRPAMLDNEADGNKMTIELSDNENPWTI FLETVDPELAASGATLPKFDKDHVMLF LKMYDPKTRSLNYCGHIYTPISCKIRDL LPVMCDRAGFIQDTSLLIYEEVKPNLTE RIQDYDVSLDKALDELMDGDI IVFQKDD PENDNSELP TAKEYFRDLYHRVDVIFCD KTIPNDPGFVVTL SNRMNYFQVAKTVAQ RLNTDPMLLQFFKSQGYRDGPGNPLRHN YEGTLRDLLQFFKPRQPKKLYYQQLKMK ITDFENRRSFKCIWLSQFREEEITLYP DKHGCVRDLLECKKAVELGEKASGKLR LLEIVSYKIIGVHQEDELLECLSPATSR TFRIEEIPLDQVDIDKENEMLVTVAHFH KEVFGTTFGIPFLRIHQGEHFREVMKRI QSLLDIQEKEFEKFKFAIVMMGRHQYIN EDEYEVNLKDFEPQPGNM SHPRPWLGLD HFNKAPKRSRYTYLEKAIKIHN
12914	26815	A	13049	30	477	VRAEHCAVWERNFEETVRWTSVKFLMTS PEIASLSWGQMVKGSNTTYKDCKWPG GSRTWDWRETGT EHS PGVQPAAC\DVKE VVEKGVQTLVIGRGMSEALKVPSSTVEY LKKHGI DMRLQTEQAVKEYNALVAQGV RVGGVFHSTC
12915	26816	A	13050	179	389	NIETIQSMFPI/DNEMKLEINLKKATWG IHKYASQVLWFMP I FPTLWEAKVGEFLE PRSSRSVWETWRDPI
12916	26817	A	13052	466	1489	PGKGEMRTRSPSPLAIVPRFQRASRPLL CAVSPMASASGATAKHEQILVLDPPIDL KFKGPF TDVVTTNLKLRNPSDRKVCFKV KTTVPHRYCVRPNSGIIDPGSTVTVSVM

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						LQPFYDYPNEKSKHKFMV/QIFAPLNTS DMEAVWNEAKPHELMDSKWR/CPNENDK LNDMEPSKAVPLNASKQDGPPTQPHSAS LHDTETRKLTECKRLQGEEMKLSSEENQ HLRDEGLRLRKVAYSDDKPGSTSTASFRD VTSLLPSLLVIAAIFTGFLFFFWRRSL TLVAQAGVQRRDLGSLQPPSPGFKQFQSH LSLPSSWDYRRPPHPANFCIFSREGVS PCWPGWS
12917	26818	A	13053	892	189	SYDPGALGCRPAPRSRGKSGSGATRDMH PMSRERAKFVKSL\YCKTTRELMHAR CCLNQKGTILGLDLQNCSELDGPNFHQ AHTTVIIDLOANPLKGDLANTRGFTQL QTLILPQHVNCPGGINAWNTITSYIDNQ ICQGQKNLCNNTGDPMECPENGSCVPDG PGLLQCVCADGFH/GIQVYAPGLVLTAY VLRDSGSHHSIRLHSALGDPAPKSQDFM NYIGLTIDLRSI
12918	26819	A	13054	423	12	SFNQKNPLRQKCSLRPTRPASQSLATWP GQSTRFEQALPWALWDPQSKRAE\MQL EPPHAHTWTHTAHTCGHTGA\FCSAHTEV YVHLHSPVHAHTHAHTHSPPVHTCGCRL HAHTH\PQTPSPPGLLSLLAVARPQS
12919	26820	A	13055	16	349	RRSGKNDPWTQSPRAAASHTRCPHBAV AAAAMPKRKTEGDAKGDKAKVKDESQKT S/ARMSSKSAASKAYAKPIKAPAMNGEN VPNGIQRKLEAFYDLQACRHLTRLIDFA
12920	26821	C	13056	716	594	MMQTETGVMPPQARQCLEPPGAGTGRKD SPLYPSEQSWPL*
12921	26822	A	13057	353	2	IGNPGKTTFNKPPPPKFFFSKFFMFLF FLVKTRSCYVAQAGLQTPG\SSDPSASA NQSAGITGVSHHTQSEILKYTVFCLTFQ TPEYTIPTWSIPCCSHFSCYLCFLFAC FLRQSF
12922	26823	A	13058	864	529	EVSTSKTAGCRGCALVISMLCIIFFQGL FTRALLRITCSALLHADWPEISFVVVVVF FKTESCSVAQDGVQWCDLRLSKPPPP\G SSDSPASASPVAKITGMHHHARHGLKS
12923	26824	A	13059	2714	1376	GRYDGLVEQLGGRATPAVGFMGLERLV LLVQAVNPEFKADPVVDIYLVASGADTQ SAAMALAERLRDELPGVKLMTNHGGGNF KKQFARADKWGARVAVVLGESEVANGTA VVKDLRSALAVGVILGVCALIGWRYWNS HQVDSARSASLAYQNAVTAVERSEKPSI PAAEKFAAENKNTYGALASLELAQQFVD KNELEKAAAQLQQGLADTSDENLKAVIN LRLARVQVQLKQADAALKTLT/TPIKGE GWAIVADLRGEALLSKGDKQGLLSVTL LSGCSLFNSEEDVVKMSPLPTVENQFTF TTAWSTSDSGIGNFYSLNHPALADNVV YAADRAGLVKALNADDGKEIWSVSLTEK DGWFSKEPALLSCRVTSPVWPNQTEKFN KQRTGPAVAEPEQAGVRRHYLYPFTGG YRRRRACQAEPAARCAATEEHGSRN
12924	26825	A	13060	99	254	RNHLVAFKELSALKVKVRVDWAPWLMFV IPAF/LEAKVGRSLEPRSSRPAAWT
12925	26826	A	13062	127	386	FSYYYYFFFFLFLCVFVIPGEPFLKMKL GPKPTIMLKEKKGGESYSELFETDQME

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						WL/TPVPIPTLWEAEVGGSEHRSSR
12926	26827	A	13063	1	209	GKYILLKLVFCCFLRQGLCHLAHCSRL PGSSDSRASASQVAG/ISITGVHHHARL NFVFCFFFLVCF
12927	26828	A	13064	132	1	SHAMCCNYLKRFGWARWMLPV/IPALWE AEAGRSPEVRSRSAL
12928	26829	A	13065	269	134	TLWSVFASS/WAWWLTPIVILAPWEAKAG GSPEVRSRLRICKQKVLS
12929	26830	A	13066	853	461	RLWRSVSQFLCACVHMCVPSVCVCGLAH AGTYAVSTCVH/MCVCMCARITLAKI CSETSGNLLFRKIISLLDLFTLNFSIKY KVQLVLKSRSLAWWGRIKLLTLSPFSD VNTFERINYWLINDISIIR
12930	26831	A	13067	57	2066	AQPTGRQTSTVAPTATARSRGGRVPIF PCPHAPATLLSTSRVTPASPAASKAL RLSASALFCLLLINGLGAAPPGRPEAQP PPLSSEHKPEVAGDAVPGPKDGSAPFVR GARNSEPQDEGELFQGVDPRALAALLQ ALDRPASPPAPSGSQQGEAEAEALLT ETVRSQTHSLPAAGEP/EPAAPPRPQTP ENGPEASDPSEELALASLLQELRDFSP SSAKRQETAATAETETRTHLTRVNLES PGERVWRASWGEFQARVPERAPLPPPA PSQFQARMPDSGPLPETHKFGEGVSSPK THLGEALAPLSKAYQGVAPFPKARRPE SALLGGSEAGERLLQQLAQVEAGRRQA EATRQAAAEERLADLADLLQYLLQG GARQRGLGGRGLQEAEEERESAREEEEA EQERRRGGEERVGEEDEEAEEAEADE AERARONALLFAEEEDGEAGAEDKRSQE ETPGHRRKEAGTEEGGEEDDEEMDPQ TIDSLIELSTKLHLPADDVVSIIIEVEE KRNRRKKKAPPEPVPPRAAPATHVRSP QPPPPAPAPARDELDPWNEVLPPWDREE DEVYPPGPYHPFPNYIRPRTLQPPSALR RRHYHHALPPSRHYPGREAAQARHAQEE AEAEERRLQEQELENYIEHVLLRRP
12931	26832	A	13068	282	53	PGFPQGGKFRFKKILPQDYPFGGAPNSK ARPGQGVPPGIPA/LWRVKGGPLRSGG PGPPGAKGGTPFLPIPTTKKS
12932	26833	A	13069	177	2	VSLCRPGWMECSGVISAHCNLRPLGSSN S/PALASRVAGITGARHHALLNSLFKVL SRA
12933	26834	A	13070	789	302	PHPEFYYSFQYFYFFISFHFTRHFIVH YFISSHFISCHLASSSSSSSSSSSSSS SSPPAFHYSFHHFISFHLAIHY/HFIIIS FHLFHLFSSFHSISFRDRDLLYCPGWSV PPHPAFHYSFHH/VHVMRHFILRQTRS IAQAGIQWRDLCSLQPEVGSRSA
12934	26835	A	13071	193	2	PPYLKSHSQVDLSPGVQDQPGQHRETPS /LTKN/TKVSWVWCTPVI PARWEVEVR ESLEPRCSTRA
12935	26836	A	13072	122	1495	LLSDFFFFETE/SRSIAQACMQWCYLSS LQSLPPGFKRFSCLSLPSSWDDRCPPPC LANYCIFSRRDRLPCWPWSRTPDLR
12936	26837	A	13073	178	347	CCLCNDNSVLLCMYLLVCMHACMHALY IKTWK/MQLGAVSHACNPSTLGGQGEWI T

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12937	26838	A	13074	165	34	FILSFPFETVSFYFVAQAGVQW\LIIAHC SLDLPRSSDSPTSAP
12938	26839	A	13075	205	105	GGWVQWFMSIIP/AIWEAKAGGLLEPRN SRPVWAT
12939	26840	A	13076	3	357	HEREYTQAEKRKFIAFFFFKMGSCSVIQ ARVQRHDLSSLQPP/RVAGTTGTHYHTW LIFVFSRTDSRLPSSPRSPLTSVISLII PLSLIPTTYLTTPSRPSSTSPPSHPSFR APLTSDP
12940	26841	A	13077	3	477	STPALTARGLSGGSRASVAAMVLESEQ FLTELTRLFQKCRITSGSVYITLKKYDGR TKPIPKKGTVEGFEPADNKCLLRATDGK KKISTVVSKEVNKFQMAYSNLLRANMD GLKKRDKKNKTKTKAGSNSS/ATTAAP AAAATAATTAATTAATAAQ
12941	26842	A	13078	1077	1566	RQVTSLDPLKTFPRTSLEFTSPTGQLDS GATAFTVVWPSGAPTPRGRESAAHQGN/ YPVGQRS\RMAGLSPRSFCWWEVSFSR/ SHSC/ICWVQLGKSAVLEQQSRGPGAHE GSRRRGGSSPPCPPLQTQLVFSQPQLSM SAPIHRLSVTLQGDCISTGGAPSRCLRA
12942	26843	A	13079	3	396	HERGRKMVSVT\RLIQLRLNWSAGHDLO GKLQLRYQEISKRTQPTTKLPEGPSHKL FNYYY\CTRDGRRESVPPFIIMSSHKAL VSRMPAYSFAEAATDKKAVTPAPSIYRG EQSSDHPYLRHCTLTVTRL
12943	26844	A	13080	467	109	SLVPVVSPhLKEPSCRVLINVMVLVPEKE QEFWSKEAGSLFSPVPVFCWTPSIVFS SSFFFLFRCVCFEEEECFEEEE\LLF FGTKKALYLLRARGCKQYKNQKLIWYLT FLSLLVK
12944	26845	A	13081	458	51	VSLFCTVAPLLLLPEGIFFSCSLLEVKA PMRDVSGVFLTLFLYSLVFFPLGVFFFL FFFLILPPPKIFFFFFCVALFFFSFAF GAVFLF\SLWSSVLPVGVFFFTACSSFFF FFFFFFFLRQSFALVAQARMQWR
12945	26846	A	13082	23	327	RSDSEGGRRGHKYIFIPYTHTYHTYIFT YTOIYICLHIYACLS/LICTHIFISYI HTYIYISYAHYIYLIHTHYLHIYHT YIYIYLIHIYSSWVCKGS
12946	26847	A	13083	352	153	KKLVEYYSAIKKNSVLH/VSTMRLKN ITLSLKTQSQRHLYYIIPSVRNQVRQV HKYRSRLVDS
12947	26848	A	13084	121	417	DYDYCYCYYPKIYLTCLLYFY\VGNYIY THIYVRHVYICETYPVYTHIHTYICIIY IYIWKETTWLFSCGISKTYRTHDLAYTY LVFCLTHVTFHVSST
12948	26849	A	13085	242	12	LSSRLPMLLETKEITSKILPSRKL/LPY GWCFKSFKITWVSQIRNRL/AQWLTTVI PQLWEA\SGLLKPRSRRAWTTW
12949	26850	A	13086	274	340	GGEKKTGPGFLEKKSFFGGGIFGPPP/P TKRGVFPSPKFFFPKTKNFGGGGP KIPPPKDFFSKNPPGVFFSP/YKKKK IIFPPPVKLGPDKFLKSPPPFFFFFYF FFFFFFSSQEVNLKALSSTSEIIFFYLV
12950	26851	A	13087	241	405	PPPSKIHIHGNFRKMSDVKNATGWAWWLT PVIPARWEAEAG\VSRLPRNSRPAAW
12951	26852	A	13088	537	375	KHSLTSLRLLECRGTILAHCS/L/CTSL

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						LGSSDLSLQPQQIAGTTGACHHTHLEKIF
12952	26853	A	13089	448	186	GALVFPSSQAPPCCPPKMEQSF F F F F F F L ETGSRSVSKAGVQLHHGSLQPPPPGFER SSHFSVTTI/TYLYHHRLLALHVLFELHIN GIMHR
12953	26854	A	13090	365	191	GQEREKEREREKRRQKKREVE/REEEKE RVRDLESESNRALERERSALVDRAPLSR PG
12954	26855	A	13091	148	316	DKMESCSLAQTVQVHDLG\YLQPSPL GFKRFCLSLSSWDYRWETSTEPFQQAV F
12955	26856	A	13092	712	229	FVAWVKMAEYLASIFGTEKDKVNCSEFYF KIGVCRHGDRCRLHNKPTFSQEVFTEL QEKYGEIEEMNVCDNLGDHLVGNVYVKF RREEDGERAVAELSNRWFGQAVH/GEC TRGGGFCNFMHLRPI SQNLQRQLYGRGPR RRSPPRFHTGHHPRERNHRVFP
12956	26857	A	13093	835	405	ELIERLGPNQKPPILMWKPMPSPSNMKA SAALLCLLLTAAAFSPQGLAQPVGINTS TTCCYRFINKKIPKQRLSEYRRTTSSH PREAVIFKTKLDK\EICADPTQKWVQDF MKHLDKKTQ\TPKLLNIHDWNLENQAMT LRKPN
12957	26858	A	13094	1137	424	LCPSHFAPTTLTQPGAHKNMCCIKSRFK RDLGLCRTCLVNKMTSSILGKSHRHSL VSINQGNALWKAAG\PLSWKAGYC\QG FSPCDLKYG\SWDEKDLTVPQPDTHKG SVLRWISKRGKPLAVEIBGRATGLPGLA PWGTE\CLGYKTPIV\HLENSEMG\ENR PYGGEARHVCNAALLFFTPLRCLGGEK HKSGLRAHPVIVLSLELNVDIDSFAHMF FADLLLIITLLSCYIPFC
12958	26859	A	13095	1	324	ARGERERERERERERERERERERERE RERERERERERERERERERERERE RERERP/RPRVLFFVRGREGSHPEKCN KKERAPFSRALRKISIETRGGVSITTEA CVFVIGAHVRCSRVIYI
12959	26860	A	13096	508	840	DGVSLCRPGRTADCSGAISAHCKLRFP SRQSPGLSLPSSWDYRLKPMRPANFFF CIEFF\VKTGFLVSQ/AMGLDLLNS/SI PRLGLPKCW\DYRREATAPGQELLLNR TGM
12960	26861	A	13097	53	254	WPQTASCLVAQAGVQWSDHSSSLQRQTPG \SSHPPASASQVARITGMHHCWLHLII LLRAHGSSPLC
12961	26862	A	13098	329	67	GPGAPLLKGEKLLPKPEPPRISPIVSAF FAWGPPPGYCFLLKKGPF\VFPPSFFG KKKNSPPPHINGGAKTFPNPPLLFSSF FFF
12962	26863	A	13099	253	444	EGAFSLGTFFYFIFFLVLSNTFLLSIKNQ QIWNKKTW\PSFPLTLIALTLLLPIS PFILII
12963	26864	A	13100	341	590	PMASQICIGRIPPFLYLKWYFPGKV HTCNPKTLGGRGALITQGQKFENSLAN\ MAKPHLY
12964	26865	A	13101	55	184	RLREPTPLYSE/HAPTKYYRMAHHNYPH SPPIQPQRHHYRVFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
12965	26866	A	13102	433	762	RNLLNCKRGLERKGCASWPVPLFLQR RVWPRPTAELNEACMLAQHNCQNVKME YFQLSFTKRQEI/WLGVVAHACNPSTLG G\QGGGIACSQEFKTI PSSKVRPCFYLK
12966	26867	A	13103	349	250	DLFFSTKPPPPPPPPKNLGP\GPFPPP FQEG
12967	26868	A	13104	3	236	YPQHYPSCPTFYTLTKNHNFLIFFEV GSCSVVQARVQWCHHGLQPP/NSSDPP ASAFQVAGTPGVSHRAPKQNF
12968	26869	A	13106	154	4	KKVKNTVHYNGKYFLKSQNSTFLKEIL /WLGVAHTCNPSTLGGRSGRIT
12969	26870	A	13107	391	150	RPPKKPNKKYSQITSKGIMVYTRKYL TKKKAMSQALWY/V/HAVPATQEAEEVGG SCEPGSSRPCTMIMPMTNTHCAPAWAT
12970	26871	A	13108	90	252	KVGDGGRCLVFCFYFKRQGFVTAQAGVQ W\ATIAHCSLKLGLSSDPQNYEDSWGT
12971	26872	A	13109	197	414	LYEFIKITVLLGLGCPGRYGCNSQRFF SLEMEFHTVAVARVQWHDLDLQPLPPR PNRFSCLR/YPQSSWDYR
12972	26873	A	13110	2	317	GRVGANVHKGHRQRTYGSVIPHLPLHV LKKTFSLRDFHFSVSLKK\NLVLTCLHL FL/GVTRPRNDPFVSMMLLFTAFDRPS TILGTGLLYTEGLTVALRLAYLR
12973	26874	A	13111	413	162	LILLPQPAECLQLQASATLDCGLGPC RDCRRSLVHSLVNGAQAGVQWRDLGSLQ PPPPS\TCLGLPKYRDCSLCPAATPSGK
12974	26875	A	13112	40	296	ESRLSALYIYHICVCVYNREHLLYGIHM /SIHTYTHTHTHTHIYHMRFALEDKF ICSLLCSRQDNAFILVSVKLQRKNYFLT RR
12975	26876	A	13113	2	288	FEPRCKNSARGKVPRGFSPNLPHTVET PEGSKTGFELESR/RRHRQIHSSAQCP LTAVPGAGDAIPEDASGWHWLPPLHAQNC FLLYIQAPEQPPA
12976	26877	A	13114	685	340	LSPFRAGSARPTGPPTDAPGQRSTWTCG ALKPRRRALRDAENLFQELQEHFQALT ATLNLRMEEGMGNRIEDLQ\NVNDL\MV QAGIENSIKEQMLKTVTANMSVFGDGAS YRSH
12977	26878	A	13115	65	3021	GVLTMGDEKDSWKVKTLDLILQEKRR KEQEEKAEIKRLKNSDDRSKRDSLEEG ELRDHCMEITIRNSPYRREDSMEDRGEE DDSLAIKPPQMSWKEKVHHRKDEKRKE KCRHSHSAEGGKHARVKEREHERRKRH REEQDKARREWEROKRREMARHSRRER DRLEQLERKRERERKREQQKEQREQKE RERRAEERRKEREAREVSAHHRMTRED YSDKVKASHWSRPPRPPRERFELGDGR KPVKEEKMEERDLSLDLQDISDSERKTS SAESSAESGSGSEEEEEEEEEEEEGS TSESEEEEEEEEEEEETGSNSEEASE QSAEEVSEEEEMSEDERENENHLLVGKN LPGDRVPVPESRFRDRSGESEEAEEVVG EGTPQ\SSALTEGDYVPDSLPLSPIELK QELPKYLPALQGCRSVDEFQCLNRIEEG TYGVVYRAKDKKTDEIVALKRLKMEKEK EGFPITSLREINTILKAQHPNIVTVREI VVGSNMDKIYIVMNYVEHDLKSLMETMK

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						QFPLPGEVKTLMITQLLRGVKHLHDNWIL HRDLKTSNLLSHAGILKVGDFGLAREY GSPLKAYTPVVVTQWYRAPELLLGAKEY STAVDMWSVGCI FGELLTQKPLFPGNSE IDQINKVFKELGTPSEKIWPGYSELPVV KKMTFSEHPYNNLRKRFGALLSDQGF DL MNKFLTYFPGRRISAEDGLKHEYFRETP LPIDPSMFPTWPAKSEQQRV\KRGTSR PP\EGGLGYSQGLGDDDLKETG\FHLTT NPGGLLPRGPGFSLRVAEVS ELDPVIGR NSAGDHRRGYLPANWCDGTRNSSSYFVL PCFVVFVFLVCKLSRIKSFSLLRKELCF LRDLPRARVGI FRGAHVQGHKPHHPL PLSTRTGLGWAVIWKGTGGS RVDCLIFG AGDLFLCWDERCPLAPTHSSRPALSTTS PRPPTTQPQLLPAGLEQVFYKYKVGVLK CIKIFFEE
12978	26879	A	13116	469	202	MIITVGLCEYTKSAVLVQHS DPLPPAPG VFFLAVLDVVDIKIVVHPVFC LFVCLYE MESCPVAQAGVQWRDLGSLQPPP\PGSS TSCF
12979	26880	A	13117	193	383	AARMASTFFVFWFWFSTF\SLYSICVCV CVCVCVCVCRMHTVQLYFFQVGCQCSSL LNPLFPMN
12980	26881	A	13118	146	350	HYLVKFLLLAHPGSKAPPLNTLQPPPLA TREQPPLTVIFHYPPTSYKMAP\PYLPS LTLFGLSPAPR
12981	26882	A	13119	124	254	HALLQTLRDL SQAWHALVIPATW\BAE AGGSLEPRSSRP AWAT
12982	26883	A	13120	150	45	SLRLECSFTVLAH/C/NLHLLGSSDSP ASASQVVGGI
12983	26884	A	13121	336	446	IPLKISSWAQWLTPV/IMPAVWEAEAGG SLEVRSSGPA
12984	26885	A	13122	181	39	QNLTAQDGVQWCDLGSLQPP\LPSSWDY RRESLCPSSFFIFWKRWGFT
12985	26886	A	13123	463	2	GPAVPSGLYLK GKPMRRLCASHSPESH HDKGGQTLPRIPQ/PLCEGGSR/PLAW GAVAGLPSNRPRIVPLPAPTRSGTRVRP HTGHQPGMSEPGCGCESKWP HSAANPEA YPHFLLPFPTQGCEVLGFLYTADPWVI CVSLLPSCP NSTAVDDV
12986	26887	A	13124	429	263	DHFSFLCVTGSQSVAQGVQW\LIIAHC SLKLLASSDPPASVFQSTRITGPFLSFT
12987	26888	A	13125	310	486	NKKTTRGESSKQRQPRVSHHPGWGT VAP SGFTAASAS\RARVILLPRPPE
12988	26889	A	13126	124	461	GSPLQLLPSPLAALTRDCSEAPMGSCSV AQDGVQWRDLGSLQRLPPGFEPFSCLS P TPAP\FPSGWIDYR
12989	26890	A	13127	2	337	RGAAPAAAVTALAARTWLGVWGVRTMQ ARGFGSDQSENVDRGAGSIREAGGAFGK REQAEEERYFRAQSREQLAALKK\HHDE EIVHHKKELERLQKEIERHKQKIKMLKP
12990	26891	A	13128	681	422	CRSDRWAKEHRGKRGQDSSKDVMARLME APKQTAQYFFIFYFFETKSYSVTQAGVQ WLDLGS LQRPPPG\SSDSPASASCAPQ TAH
12991	26892	A	13129	299	579	LVMFCKVTKIERLNLWRPGTVAHVLSQ HFGRPRWAVHVGWGVDRP/RLTQHGETP

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						SLLE\NRNISQAWWCMFVVPATREAEAR ESLEPGGQRLQ
12992	26893	A	13130	268	438	KVDKSMKMRKNRPKNAENSKNKKASSPP NDCNSSPARVQ/SWTENEFDKLTEVGFR KW
12993	26894	A	13132	1108	1529	KIHSSFVLLNAKLVAVAAKTPKFYKKKT DLPQTYHSAQTAVPEIPVSAHSTFIRSF IHSFIFETESYSVAQAGIQWHDLPSP GS\SDSP\ASVSRVAGTIGVCQQAFLFF V\FLVET\GSFPHLSPLTMIRNNKKQLFK KGH
12994	26895	A	13133	497	370	RPSTVSPRLECSGLILAHCS\LDPPASA SQTAEITYGHHAS
12995	26896	A	13134	217	373	CNHTETIYVNNKKHRPGTVAH/SLYNPS TLGGQGGLITQAQEFDTSLGNMTLS
12996	26897	A	13135	257	507	PVSPGFPPPL\CPVPHTPHLCPPCRYPES PGQPAAQHCGAPRQPQNPACSSRGLF RCPPACHHAPSCLLCVCPPLPQCCRVQG
12997	26898	A	13136	137	309	PSFPTHQPFCFLFCFLVFETE/SSIVA QAEVQWCDLGSPPDQSSASPPSASSLPL SIW
12998	26899	A	13137	297	419	GGSAVYYIWEIVQVLWLPVIPT\WEAY AGGLFEPRSSRPA
12999	26900	A	13138	213	492	QVGINYQPPTVVPVGD LAKVQRAVCMLS NTTAITEAWGLPGAISAKCALVHW\YV GEGMAVGGEFSEAREDLAALEDYETCGPW NPVETEAERR
13000	26901	A	13139	246	534	DRVLPPLPRLECSSAILGHCP/APASQV TGTTGTHHHHTQLIFLLYCWLCPPLASE ASAESPPPLPRGFLCFSSTTSSITAIPA TTRDYVDVSRSGS
13001	26902	A	13140	1	206	SLEWPPFFFSFSETGSHSFTQAIQWCNH SSL/SPTSASQIAGTTGVHNAQL/VFV FCFAFMSPQLNSNC
13002	26903	A	13141	164	582	GLVLVNLVLRSLMVFIYINSRLQVTD ASRRERENESSWFCRSVCRM/PPVGP SCVHPCSPRGSISPCTPHCPLKTTQAPA \PPRPLPRVGPGLDQSCCVAARPLYD PILVAHSSWPAPSPVPVPQEDTEHGA G
13003	26904	A	13142	235	367	LALNTFCWLGVVAHACNPSTLGGQGEV TRGQE\QANMAKTCLY
13004	26905	A	13143	91	403	GALQPATAPWEPLSGLAEAGAI SPCLOG G/SGGRGASENRGCTRPGRVPGRRILNR PRAWSSWPAPPAGSERPSAINCPRAEE CGRRVWDQAALPAAPAVPV
13005	26906	A	13144	558	147	GHSFQNWLLGCPLQLQRHLLHPPDASEE CGSPFWTPLRPHIHPAGPHGSTHK\HA GGCLFPLRPSPTHCPGPPVPLPWSQ\QA PLCPHPPHSPHDWECDPGKSALIPPA AQSPSRLIKHAANEPECSPRNRRPGIP
13006	26907	A	13145	321	421	GCAQWLTPV/IPALWEAKAGESLLFRSL RPAWAI
13007	26908	A	13146	3	398	IELLQSHDKTLTDKLLLLDEQRKWFLE MESTPGEDVNNVELTTKDLEYHINLDD\ KAGFERIDSNFERVSAVG/KMLSNSIAC YREIFHERSVKVANFTVAILPQPHKLSV TINLI IQQPSTLRQDLLLLAKR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13008	26909	A	13147	228	261	SKTQRSSEYYSLSVCVVCVVRVCIYIYI FFFFETEFLS\APOAGVQRCDSLRLRP PP\GSSDSPFSTSQSAWDYRREPQRPTS LHYFVQLKHNLRVVKRRDLRNTTR
13009	26910	A	13148	3	275	KHLSDLQILRLGLSSKTRKTRYSHFAQG RSIFFLLRPSVDWIKPACMDGNLLFSKF TNLNVNI\TKKHPHRNVQNNVWPNVWAP WPKEVDT
13010	26911	A	13149	218	382	AWDHIKLESFYTAKETT/RMKRQPTWEW KIFANYPSEGLVTRMYKELKQLYRKKI
13011	26912	A	13150	391	29	FCFLFLFMFLFFFEMQDGVQWCNLSPPQ PPPPG\SSHSPASASQVVEAENCLNPGG GGCSLGDRLRLPQRKRERERETERKRKR ERASCAFCGAITFVNMWCQKHHTCNHLP WLTVFETNKL
13012	26913	A	13151	351	157	FGYSRFLCVYINFRTNLSTINYICTIYIN LYL\NIHTYTLIYTVVHTYTHIHIFYIY IGILTGIT
13013	26914	A	13152	402	111	TFFGGEKPPFTLRPGPPRREGGGGPPGP REGGFFRVPLGAFGPSRPK/RPEKSGPV WAPQIFLWGGKSRAIKESGKGFPSRIT LLVFATEKKKKTTLF
13014	26915	A	13153	310	141	REHEKQKPLSQVRWCTPLVQAAQEAEG GELEPRSSRLQCSMT\TPVNSHRPPARV T
13015	26916	A	13154	153	21	LNKCVISWLGAHAHACN/PSTLEGRWIT QGQEFKTSLGSLAKPHLY
13016	26917	A	13155	429	275	SVDIPLEKTLINKDVFKBAAFKCKVS/R QARVKFKKRYKPKVKTWFFQKLWF
13017	26918	A	13156	303	42	YRERAPVYPIIINIAFGPHKQ\TRAHTH THHTRMHAHTHHPAIIPAFANGLGT FHHKGRTYNDKVKPRLSCEAAIPSNLKS REFR
13018	26919	A	13157	198	13	SHGVAILLFFHFLNKRAFT\YSPAMNSS LCEIQEPSLG\SGSGPLSGNRMSSGKGR KYFAKI
13019	26920	A	13158	192	2	ISNSHRKDIKDPEVLLIEQKYILSGQMQ WLTPVIPAL/V/EAEAGRSLEFRSLRPA WATDRDSVSK
13020	26921	A	13159	40	190	RVDPRVRESRSVAQAGMQWRDLGSLQAP P\PGSRHSPASASQVALFLNRK
13021	26922	A	13160	1	178	PTMVLSPADKTNVKA/AWGKVGAHAGEY GAEALERMFLSFPTTKTYFPFDLSHGV SSYL
13022	26923	A	13161	411	41	ESLQICVGLHAKPSWDACRPWLQAWFR YFLLTFLGPLVFLLVFVWFSKIYFLYHLK NPSLSSCYNLD\FNTQYLKYCKKKRLG AVAYACNPSILGSQGGRITRQGFETRL GNMAKPDWVDP
13023	26924	A	13162	372	218	FWKRSWISKKGLFKRGVSLSLSL/CDT HTHTHTHTHTHAHSGYLCVLRKVK
13024	26925	A	13163	247	89	QGLVLSPWLKCRGGITAHCGLLGSSHPT TSA\QVAGTTGTQHHAQLKFFILIIL
13025	26926	A	13164	122	409	FPSTAIANSH/CSSPQGCSAYGVAIRLF LRSSNKLAL\LYGLAL/NSFFCNFQEPS \LGSLSGPLSDNKSNNLCCFKSPSSWLF AIAVLGNYYSLNTRVSGRRDGPDPNACS
13026	26927	A	13165	69	313	PSVSLFFPPNHNIIVHMLLKINSIFGE

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						GLALSSRMESVTTITVHCGLDLLGSGGP PSAAS/RVAVTAGTCHHSWLMFLSFV
13027	26928	A	13166	310	26	IKSMTPLPALNVSLSYLLPPLRPCRERG MVQDRFFCFLFCCCCFIFSETGSHSAAQ AVSQNKKTGWAWWLTVPV PATHEAEAG \ESLERGRQRLQ
13028	26929	A	13167	296	68	KNGPLNLATKSLILTMKCLGVVLGGKP NCSKLKKNKIKTKKWGWAPWLTPIPLPA/ LLEAEAGRSLEARNLRPVWT
13029	26930	A	13168	2	235	GATPCPREPSLFLPLAGWAPLSCWAPPPH CTQGTTPPGMLGTG\APIAIIGGNARSP PMFPLPLSGTRRALSQAECPTF
13030	26931	A	13169	248	406	TERCGFDLLSLGQVQWLTSTVIPALE/EA EAGELLESRSWRPAWATWQNILSLKK
13031	26932	A	13170	33	308	NSLQGAEMAAQSSLSFASSEG YRGERGR GRGRGRPGRG/RSEGRGGRGRPGRGGRG RKVLLLRICVWRRVRLWNRGRIGVGGR VTYLMSEI
13032	26933	A	13171	294	56	ICKRNYLFFIYFLREGLTLLPRLECSGA ITAQCSL\GSSDPPTSASTVSGTTGACQ CALSSRDALISLCYPGWQAAPGLK
13033	26934	A	13172	71	476	DSLNYDNHLYQMPLIYINMGLAVTISLL G\ILVYRSHLISLLCLBGIILSLFIIA TLITLNTSHLSLNIVPIAILVFACAA VGWEECGFRSRPTALILEGPLRSCQPR CVRPACTRRGPAFVGKNRHSIGG
13034	26935	A	13173	86	318	NNCNVVCVCVCVCVCVCICIHICIYV/YV YICIYTYKYICITYKYICICVYIHYM YMCVYVYICICMCVYICIDSKGR
13035	26936	A	13174	466	726	NCMKFGAVTRIG\DLFWINPLSSCSLL REKDPPTTSGPQTDQPKHLTNFKSGKR PLFTLFSNLPHYPSTSFBSQSWRHTSIS PFS
13036	26937	A	13175	128	325	FLRVILICHKMYGCVCVCM/YACICNGM CIYMCVCVKS WKLPKELKCLCISDEVGW VLTQWAGREEN
13037	26938	A	13176	134	311	INSNSEKMGSHYVAQDGV/WQGLFTGH GIAHCNKLKLGSSNFSASISQAGTTGI VANG
13038	26939	A	13177	577	1052	SPTSTRTGSGVAMWLSQPMGRT\CRSKV ASKSRLHGPLIAHPPVRCPLRHHY\ KAQAGRGLSLEE\LRVAGIYKKVAQTIG IS\EDARRNQST\QALQAKVQRLK\ED RSSILFPRK\PLAPKKGDSSAEELELD TQLTGPEMPIGNVYKEKARVIAD
13039	26940	A	13178	496	678	TLNFVWAQGLKITRPWKNAPVFPVW\R LRRKNLLTLKGEICSDPKWPYCLPPWKT KKNLV
13040	26941	A	13179	192	421	GIYTFFLSFFLFLRQSLTSPRAGVQWC NLCLPGSSDSPASASRVPG\ATGT\CHH GSANFLYFLVGDVRFVGVGPR
13041	26942	A	13180	144	5	LQLATKLLKMLGVAHTCNPS/TLGGW G\GRSQGQEFETSLANIVKP
13042	26943	A	13181	351	51	KKKKKIFFGTKRRRFFFLKGVWGPPPPK VSPPPPKISPNPPKNNPLLKA/IKSPQ NWLFFFGPPSCKFFPPFLNPKNSPWEN PPSGGEFSPKKKKKSAI
13043	26944	A	13182	2	218	THFGCFVFLFFETEFCSCHPGCRAGVQW

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						RD\LAHNSLLPPLG\SSDPPTSASQSA EITGMSHHACPIFKKHS
13044	26945	A	13183	33	304	EKHGIFRAVKILCMILQRWTYATHLSRP TGYTAPRVNPKLWTLGDNVSM/SGSLI VTNTALGWGLLIRRSSACMGQGDMGNLC TFLSILL
13045	26946	A	13184	277	13	FSFFLIVEMGSCYIAQAGLELLGSSNPP SSASQSAGITGMSHHPAWLATLKRAFVS D\NSLSFPSSENAHLISILAGHFCLMGFF FFQ
13046	26947	A	13185	140	361	ITCCCVCIYTHIHTYVYVCYIYTHTYI RVCV/YIHTHTYIHIYIHVFIYIYIYT FMHTYIYPYVCMVLLQLTL
13047	26948	A	13186	64	759	CLSASAPTSTMPMTLGWDIRGLAHAI RLLEYTDSSYVEKKYTLGDAPDYDRSQ WLNEKFKLGLDFPNLPYLIDGAHKITQS NAILRYIARKHNLCGETEEBKIRVDILE NQVMDNHMELVRLCYDPDFEKLKPKYLE ELPEKLKALTS\EFSGGKRPWF/SQGDK ITFVDFLAYDVLDMKRIFEPKCLDAFLN LKDFISRFEGLKKISAYMKSSQFLRGLL FGKSATWNSK
13048	26949	A	13187	41	426	LFFFFFFESGPCWVTQAGRR/WNDHGSL QPGFPGKLGSPCLTLRSDWNYRPGMCRH TQLVFAFFFFFFPREKKFLLGAPTGFKTRG LRGPSRFGFGKGGNKGGEPFPPRAKGLIF LEPERGQAFFGVFFGPTQ
13049	26950	A	13188	39	197	FFFLFKTRSCSFIQAGVQWCEHSSLQPO TPG\SSAAPASASCKAGTTEAALKL
13050	26951	A	13189	221	396	GIQLQGAEGLDVNTNSPFCWRLYDQKTV YHECRMWANSHP\PPKGLLRDITPRCW AP
13051	26952	A	13190	2	826	PGSTISSRRRGACSGSRGHPSPRGGSG VASLERAESWSTEPAKAIKPIDRKSVMHQ ICSGQVVLSTLSTAVKKIVENSLDAGATN IDLKLDYGMDLIEVSGNGCGVEEENFK GL\TLSALKHHTSKIQEFADLTRVETFG FRGEALSSLCALSDVTISTCHVSAKVG RLVFDHDKIIQKTPYPHPRGTTVSVKQ LFSTLPVRHKEFQRNIIKKRACFPFAFC RDCQFLEGSPAMLPVQP\AKLTPRSTPP HPCSLEDNVITVFSSVKNPGPSSR
13052	26953	A	13191	235	1	SPCARQCCPENPAGQEPRRRLRGPQKW WPRSIKFPLPAV/RARFLLPSAPLRQL VSGRVGGRVGRPGKAVQVSGGLN
13053	26954	A	13192	2	386	VIYLLFFETESCCVAQARDGVSPCWPG WFQTPG\SSDLPASAPK/VAGITSVSHR TRPDVRGFKKC/GLQLEMHLALL/TT SHRFWYFVLLFSFVSKGFFIFFFPLFFF FFLGKGGFFFFPRGGGGQI
13054	26955	A	13193	749	506	GQTKAFVLSYCGASPSIKQ/PCPQAKDH PLEPSMHPEGTQLQSCSTMLGPRQLSSE KQPLLPPRSHLKSSPMLRACKGLTS
13055	26956	A	13194	73	297	RMPGFGALGSPFSCQRIECPC\AGAGSC TYASFCKCKEYKCTSCCKSECGAPPGNQ GAGQSQRREPRAQAGAGQ
13056	26957	A	13195	670	390	PRETYIKPFARSIGCQPPKTIHPTSRRP STRPPARPHARPPVHTP/APSVMHSDRP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STCPPSIH\RPPSTDVSRPQYSLSPSTS LALPGQSCCLGR
13057	26958	A	13196	2	438	LSFTSIEFCHLLFLNQLICNYVIFTKSS TISCEALGRLLVVYPWQRFESFGDLS TPDAVMGNPKVKAHGKKVLGAFSDGLAH L\PPLKPTFATVSELHCAKLHVDPENFT LLGNVLVCV/MKHNFGK
13058	26959	A	13197	57	499	SPSWPRSSARPCSGHCLLPGLWDHGKAP CLRAARHSQGHGFRKGRKGCGLWAAGV TKNPVPTWRAG/SRRGPGVTSPPPVPSV QNPP\PQRRHGGSQATRPVLFPTPPKH MEGPNAPILGDQRITAPPEILYRPPRA ATCDALRRG
13059	26960	A	13198	34	465	GILPYSPCVLRAPNSKRVRKCGCTTPRH L/CKATRKCGCTTPRAPLNETRKCGCTT PRHLSRQLGNAGALPRGHLNETRKCGCT TPRAPLNATRKCGCTPRHLSRQLGNAG ALPRGHLPLKETRKCGGATPADAFYETKK IGGGL
13060	26961	A	13200	177	1075	PTSSSMAPKKKLQGLVAATITPMTENG EINFSVIGQYVDYLVKEQGVKNI FVNGT TGEGLSLVSERRQVAEEVWTKGDKLD QVIHVGALSLKESQELAQAHAETGADG IAVIAPFFLKPWTKDILINFLKEVAAAA PALPFYYHIPALTGVKIRAEELLDGIL DKIPTFQGLKFSDTDLDFGQCVQDNRQ QQFAFLFGVDEQLLSALVMGATGAVGST YNYLGKKTNQIV\EAFAQKDFSLALNYO FCIQRFINFVVKLGFGVSQTKAIMTLVS GDSNGPTPASTCRKPPGEFT
13061	26962	A	13201	35	464	VQEFKTSLSGNVAKPCLYKKKKKSPGG GVPPPPPKKTWVGTTLSQKIRPAGPLIF PPPLPRGQQGEPLSPIKGGGGGSS\YP PPPPCLTGRA/PPSPISAKSSPSPP CQYVYHPPLPLFFFLHALRRATAPLFL FLVRA
13062	26963	A	13202	1153	259	AGGVLRLGVVTGSRMASDSGNQGTLC EFAVQMTQSCVDVAVRKSQGVAGVQDV EVHLEDQMVLVHTTLPSSQEVQALL\EGT GRQPVLLKGMG\TGQFSESGGPVAPGG GLGTVQGVVRFLLQTPERCLIEGTI\PG LEPGLHGLHVHGYGDLTNNCNSCGNHFN PDGAS\HGGPQDSDRH\RGDLG\NVGAN AAGGAFFRMEDEQLKVWDVIGRSL\IID EG\EDDPGAREGQSLYPKITRELPGSRL SCGI\IAKSAGLFPEPQSKICSCDGLT\ IWEERGRPIAGKG\RKESAQPPAHL
13063	26964	A	13203	281	420	VDGSKKYNEPVPALWEAKAGGLL\EP RKSRATWATREDSVSTKN
13064	26965	A	13204	3	1125	SDSPQTPRMRVMAPRTLILLLSGALALT ETWACSHSMRYFYTAVSRPGRGEPFIA VGYYDDTQFVRFSDAASPRGEPAP\W VEQEGPEYWDRETQYKQQAQTDVSLR NLRGYYNQSEAGSHTLQWMYGCDLGP DLRLRGYDQSAIDGKDYIALNEHLRSCTA ADTAAQITQRKWEAARAAEQWRAYLEGT CWEWLRRYLENGKETLQRAEHPKTHVTH HPVSDHEATLRCAWLGFPYPAETITLWQR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DGEDQTQDTELVTETRPAGDGTTFQKWA VVPSSGEEQRYTCHVQHEGLPEPLTLRWE PSSQPTIPIVGIVAGLAVLAVLAVLGAV MAVVMCRRKSSGGKGGSCSQAASSNSAQ GSDESLIACKA
13065	26966	A	13205	417	13	GHPRVMLQCHMGASLSIMTPPPPIRSYQ PALTRSSATKPA\TSAPSITMTPVTAN IS/VWPTANTTTTTLKSNPTSS/STLSTP IWHPSILPAPPSTPAPLTTVTNSATTST ICFHVQLFQAHHCCHCIAAALEYTS
13066	26967	A	13206	1139	559	GLSELSIHPSVARVQBGHGATPERSIPW PGGKPRRGGRGTGLREWGGGSHRSLGQT KKKGAKAKRDHCAHGPAAAFQGGPFPRAT QLLSPCHGCSWKENQPP*GPPGHACTAW EKTVTGSGCRPVTKPSDPGFVQAPGT KGNPAPGMDGCAGFRISCHPVPITKPLS NTGICVLLCYEFGFLIAIVGCWGFK
13067	26968	A	13207	306	332	ENGEIRIYIYICLYLIKHWEEAGCGSV HL*SQHLKRLKWEDYLRPGVPDQPGQHR ETPSQKLNK*INNDF
13068	26969	A	13208	48	233	GKQNHLCCLWCRLFLLSAIVSRNVYIL T*LSLSLSQCVCVCVCVCVCVCVCVAIL ENYPR
13069	26970	A	13209	250	2	YCEGDLGSSRPVSKCREFSPPRDKRIM PWPGAVTYAYNPSTLGGRDGIWA*A*EF ETSLGNIVKPHLYTHTHTHTHTHT
13070	26971	A	13210	615	120	SVFWPLLGGVSWSGYTEVRGPLEKAVCP LSELEYCAGRSAALFRAIRLFKDALSLL KLCPPPPFPLGAPLSP*EALVCVPLHV STCLS*WCPTPCPPERSWCVLFPSPMYPR VCPDGLLPVPLRGPGVCVPLHVSMCL LSLFNSLLRLRRTCGVWFSPVPLVC
13071	26972	A	13211	239	429	FILLRNKLQPGTVACGCPNSTLGSQGW IA*AQGFETSLDNMVKPCFYLPQLKKKK KIKNLGV
13072	26973	A	13212	954	503	VQLLPLCGRDLYLFAFNLPYTRCQWHFL SKPRAPILAGSDRWPCPCPFWLP*WC HVSAHAPQFPCKAPEAPLPVGCPCSPA PSLEAALLILRAGLVVLRAPFCFSAHLL SCHSQCCQFPCSEKRSCLGGRDRHAASN PLSAVWPPGE
13073	26974	A	13213	1844	1147	LHSQIYSTAKKASLSMKGSRDKTRAASS RPVPSVLGVPPWSTLLQHPQNMWPGPAQ QQGQPSGRQAWCTPGEAPGAEAAPQ*QP HPEEDHSGGPQASALALPPSPSQRDV QGETGMQGRSAPRSASSSACCACRWSRL PCPQLLQRHPGLRLVSPAHSRPPGPAPS SSSGSGLVPGYLPQKGLAGLSAGAVLCP PGLLRVAHGAGYGPSAQMLHARLSSSSL RGKRFLRF
13074	26975	A	13214	413	60	LCSKSGHGSFAMDCETLLTFPRLFYPIL HMPTVPGQALPVHTPFL*LKLPLLPGIP SCHSPFLD*AQESPPPGGLFGHPGSG VLCWFHSLKHPVLSGSSVSTPGSASPS RSRAL
13075	26976	A	13215	67	196	GLSLSSPKVTHNATLMGCIFQN*KAFVY HSMKQKKIILLFNMA*P*YPLDFGEQWP LHGSHAYSTIL*LDLFCKKEE*DEIPY

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						V*CFMLLWKSTTM*KKIILLFNMA
13076	26977	A	13216	161	2	SVFFLFIDRLRLYLKSVWAAVNSSTLGG RGRIRIT*AQEFKTSLGNGKARPRVYQ
13077	26978	A	13217	57	184	CLTVCKDKVSLCYPGWSPVV*SYLTAAS NSWSKAILPPQPPE
13078	26979	A	13218	292	400	LKVKQGRGHLDLNLQGGPLDL*SNSLPLSH TPSHRRTV
13079	26980	A	13219	186	394	YLVLSTFLFYFLFIFLSRVSLPIFFILEI *LGIVAYTCNPSTLGSQGGRIA*AQEF TSLGNIVRPPSLI
13080	26981	A	13220	315	448	KTCDLGVVDHVNPNSTFGG*GGRIT*GQ KFETSLDNRARSCLYK
13081	26982	A	13221	3	13	LRPLRSFVSVLERLWASCCLGSELVVDKT KRKKRRELSEEHKQEIKADEFELFDTKD EVIDYHELKVMIALGFDVKKADVLNLI KDYDR*VIGKISFGHSIEIVTDFQL*R
13082	26983	A	13222	1	715	VDMHSRGSPELTHASTHASGKMAAPWAS LRLVAPMWNIRIRGIHRLGAAPVPEGNQ KKKRTILQFLTNFYFDVEALRDYLLQRE MYKVHEKNRSYTWLEKQHGPGYAGAFFI LKQGGAVKFRDKEWIRPDKYGHFSQEFW NFCEVPVEAVDAGDCDINYEGLDNLRL KELQSLSLQRCCHVDWCLSRLYPLADF VAGAFRWAGCPRIFRGTAKHGFHHLQ*D LSSGWATCPGTSPT
13083	26984	A	13223	1019	1238	LTGAEYKKSDDLSTESVTANLEPEAPKVF SRLDDEAPVTVLPARLPLPAP*HTARPD PEQRRRSMQLAPARPL
13084	26985	A	13224	1534	1181	RWNSEPDYSAGGPRAGRGARLLPVPKSP GGGGAVAPGPTPLRAERTAVRLSIS* NSSTAPADPGAAPPLHPQPAEAGTWVSA FLRVIFCFPSLGFGCWEKKIAFVFPFPT DEKCL
13085	26986	A	13225	328	22	CLESFPRDRPFQGPAPFKHPPLPLAFLSQ PGKVQYFFFSNCKSLSSQEIKNRSRVPT SPPAPSPPPPFFLYFSLTAEGGEV*KET LSDRAPPSSREAPICQV
13086	26987	A	13226	180	5	NSIDYKINVKNSNRPGAVAHTCNPSTLG SQGRRIT*AKEFETSLGNIVLLIYTIY YI
13087	26988	A	13227	237	528	VGLCQDPLLLTLTDSFCSVLWGGSHLAF HKNLYVVHIDLVMYFSRISFYFTLSAAI CLSLYLGSILSPFL*LFYCAYTTLYLCL LITTLFFLIPKV
13088	26989	A	13228	140	366	NATCLWHPMSFYPTY*C*LSPGLLRWV LAITPIVLMILISSYNHVISYGGTFRS NFFLDQIILTFLIYELHIV
13089	26990	A	13229	257	25	LPASLSGRDLSAQPYSMRPPGGELRAEG QSSLCSVARSSL*LHVCVCVCVCVCART CVNVFACVLLSTKVCCLHPLPE
13090	26991	A	13230	561	52	WPSCSSSGSPMLLPPVPPGSLG**SFSP LPAAALPAPCAAPRAPLRPCGPAPT AAPAPAPAAASLSAARAAAGSPGSR PSARGARRRSGPCAPPEPRLGPRAPSS APRTRTPS*GRARSGSAGNAPSARRT QGPRAACSLARSWIWPAGRGSGCRAL GA
13091	26992	A	13231	335	103	CQKYSTSYCNKWLATLVIICSRKI*DGL

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						KGQAWWLVPVTPMLWKAEAVGLPEARSLSSPCNMARAPALKKIFLIGQV
13092	26993	A	13232	452	712	VGLEGED*PPFSPAQSQSLSCWPDCCSCP PSWPPDQRPGERPQPPDPESHGAE EEG LPERPSDA*ARPQPFSLHPGVFPQNASTQ
13093	26994	A	13233	480	2	SCFSEDWNPLKFKLQLSTSLSYRKSHTL HCAHHFRGQCHSD*AFLVFSLTCLILQVG SLRFTAGDVSPSYPEKLRVL*EGRVADF HVMARKGQQAALAILLQNARTGYVWWLT PVIPALWKAKASGSVKPRSLRQTWQNGE TRLDRGESASQSAGMTGM
13094	26995	A	13234	692	824	QIMALPFPSPVPPLVM*CKGGKIPPPP SKNPRTCVGNVTVIIKA
13095	26996	A	13235	657	872	PRGPRLDVLYACEPQLITCLELGTPLKV RFWLEVVDHTYNPSTLGDQGGRTA*GQE FKTSVGNSKTLSLKKK
13096	26997	A	13236	168	365	QESLCILQTCTCAHQNLK*KFGGKSRLG AVAHACNPSTLGGQGGRII*GQEFETSM VNMVKPYLY
13097	26998	A	13237	31	338	WYIVYICVVCVCVIYIYIYMIYI*YI* YIYIKHTVQ*H*HLAFSTFTLLCNCHHC PSLELFHYPTLTYHTH*IITPHCSSC*Y QLLFYFHLVYFVDYSRYLV
13098	26999	A	13238	714	1001	SSGVSCLNLRAGWITGVNHHIHSVLVLLKR EK*TONIITEVCLMFLLLPHLAIEATVT WPGMVAHACNPSTLGSQGRRSV*AREFE FSLDNIARPCL
13099	27000	A	13239	250	406	NLA*HGGVHMWSSASQVAGITGTRCHAQ LIFIFLVKMGFHHVGDGLNLLTL
13100	27001	A	13240	256	193	WINFISLPLSSLT*TLSCVCACVYVCV CVCLRPCVHIVGGNLKRYIVFARSVTLG CKFTHLHISLIINNDT
13101	27002	A	13241	1	257	GMDLWQMCHSLSLPLIFFFFFFSEKTRS NFVPQAGFQLRALRDP*ASREAGITG LTHHVRPGQIFKKIGTLKPTILLPLLP RK
13102	27003	A	13242	319	406	KRGWT*WLMVPIPTLWEAEAGGSPDVRS L
13103	27004	A	13243	228	56	KGAPPVLKPGYPKAAKNPTPFKPPGSKV GENPPLF*NPCPGGNPPTFFFFFFFFFF F
13104	27005	A	13244	1687	612	ILGNQCCKFDAYNALANESTMISIKLNE *VREREREKEKEKERVREKEEREKKKL TSSKGTGSTATFHV
13105	27006	A	13245	220	1	TKDPSSTMPPQPNPLLSFKSQFIFLIFL FIKKYVGWMQWLLPVIPAL*EAEAGGSL QPRSSRPATWRNPIF
13106	27007	A	13246	204	375	ASWPPGLQYELRIIKCLLHCWTRAMIFR ERERERERERERERERERE*VHLKRKGA
13107	27008	A	13247	158	2	IWVPKETFFQNFNFFFGKENNFNGFFF FFFFFFFF*DRVSLTLHPSLGYR
13108	27009	A	13248	221	3	NPSQGFPLLKIFFFFLRWSLALSPRLE* NSI*KN*KI*KISWAWRTPVVPGAWEA EPGESLEPGRQLQNE
13109	27010	A	13249	81	341	GELNDTIHVKYL*YIKVL*RNRTNRVC VCVCVCVCVCVYACTQKDLF*GTGSCNC

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						GALVRPKSARQASRLKTQKTVVIRSLKAVC	
13110	27011	A	13250	299	1	ATARLRFLHGAWWYASVVPPTQEAARGFLDPRSSRME*AMILPRTCPTASVTDKIPSLASQIHRPSRVACVILLSSHAPTEAPSRWPPSPSLCPAGSRA	
13111	27012	A	13251	106	146	LCVLKQVKQATWTKYSSSQIFAILDCMTLSSHPALKYCNYVLISNQSPNHLRL*CSGMISAHCNLCLPG*SNPASASRVAVCFKASQASVLD	
13112	27013	A	13252	217	158	LFEIFCIPFFFFFFNFFFETRSHSVSQAQVQWCKQGSQIPINFFWGKEGVLDKLILISYGNAQGFVAVTPVCTTALQPGRQSETLSQKRN	
13113	27014	A	13253	150	56	TILILLLLYETESQSAQDGVQWCDLGSIQSPPRSSCHSPA*AGVNRLRQENGMSFEAEIVLSPDRTTALHPGLQIETLSHIIITILILSTISFHQLLH	
13114	27015	A	13254	174	145	PCLKMTTYDFKSALEIAFFCFTAILRYKLLIKVTHFKWLRVAHDCNPNTLGSGGGRITWGHEFKTSLANMA*PTTRSYSQRVGIMGITIPDEVWSRTQPSHIRSGPSKVYP	
13115	27016	A	13255	179	273	GQWLTPVISAL*EVEVGGLLETRSLKQAWAT	
13116	27017	A	13256	264	382	GLKIGKGCSSWFTPVIPITL*EVKARGLL EPRSLKSAWAK	
13117	27018	A	13257	1199	1563	YLVVGPAPVPLDLEPGQAGATCGPVSHYKIFAKLWAVGSILDLMGPPE*GSFLSVFTSLCFIYGVTPPHSEQPHPASPSASGLLLKGRRAWLVSTLCIGSPAPMLTGIFPHKVYNQLFI	
13118	27019	A	13258	194	242	ILYVETGSHYVAQAGLELLGSGNPPASTSEIAGIEA*ADEFIYGVSWQDECIKSMKQVAHASIPASEVEAGGLPEPRSSRPA	
13119	27020	A	13259	322	120	GPTFVLDAFQKLCLSFTSGQQADGIIPAFPIRKQGGTQWPKPVIPTLWEAKAGRFL*PRSRPAWAT	
13120	27021	A	13260	237	1	TSKKISLGWVGKQIGPTWEG*AKRPFEPGKPRVQWTVQVPALDFSLGGKARLCLKKKKKQKQKTLKLC <th>THSR</th> ITYSRA	THSR
13121	27022	A	13261	52	318	SAVGIIHRCDDGSH*P* <th>TEH</th> KQLSFLSLPSSWDYRGITRELFRQFPWIFLQLITAVISSESTVLKNLELAAVRGSHVRVIMMAVPINPF	TEH
13122	27023	A	13262	274	1	KKKKNSPVWWVTPVIPGSPG*AGELLEPRQKVQLAQVVPPLAKVVPQTKVVQGCPLALQPGEHQGI FVSQKKKNPKTKRKYWALFCSLPSC	
13123	27024	A	13263	717	877	NSTKEMAHWPGVVAHTCNPSTFGG*GGWIT* <th>AHE</th> FETSLPNMVKPHLYKKYKK	AHE
13124	27025	A	13264	288	131	SLYIWHSKRLITITNNKISGVVWCLPVV SSTWEVEAGGSLEPRR*RPWATK	
13125	27026	A	13265	80	287	FMNGEAS* <th>KTS</th> ILSQAWWCAPVPAAQ*NEAGELLEPRSEWLVAWATRALRISSRGLRFRRLRRFTSTR	KTS
13126	27027	A	13266	3	241	VGLFLFFFETESCSVTQAGVQWCGLS*L*PPPPGIRDSPASASQVAGTTGTHHHTWLIFLYF**SSGFHYVGLGRSSNS	

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13127	27028	A	13267	103	359	ICVYVYVCIYVYEMRATSKDFLNQVWFS FLRTVAVLFEYLIIVL*MWLSFHIHIYI HTHIHIFIYVYTHVLIYVYIHTYSYMC HIYI
13128	27029	A	13268	172	12	SARSSQAIQIQKSVTSGQVKPQW*QS*P TPFLPTLIALTTLLLPISPFILIL
13129	27030	A	13269	2	203	RIENIRSYKNLAALFMTAKKMGTIQMPH NFEWINKMWYIHTLEH*SDKKKKKKKVN RAEIPKLIQK
13130	27031	A	13270	236	365	KIYRQGAHAHTCNPTLGGQDGWIT*GQ KFETRLANMVKPHLY
13131	27032	A	13271	371	15	QNQINFALILIIINTLLALLLIITF*LP QLNGYIEKSTPYECGFDIPSPARVPFSI KFFLVAITFLLFDLEIALLLPLP*ALQT TNLPLIVMSSLLLIILALSLEY* LQK GLD*AE
13132	27033	A	13272	2	16	PRVRTSSRSRAALELIFFFFLGPPNLPV YNGPLGRTPKGTGELDTGGSPILCVGQG RHPYWKGAAPLAPFGKGGP*GTRPLA GPIVPPKAGLQSEMPGMAPFCGSFG*PT RPD
13133	27034	A	13273	329	290	SSALVPRLECKGIFSAHCNLCMLGSSNS PTSASRVAGITGVAGQATDKTPQTL*SR SQPSHMDPVRVVS
13134	27035	A	13274	175	13	APCDHRPCPPENNPL*L*FSITFPNPIK RPHPYLLTLFSDSAHLHPGEIEQR
13135	27036	A	13275	355	861	PLTTTPAAPRAPCPSPRLSGQPLTGPT GSRRLSPNISEQGEPLALTVGHPLST QPGPTVPSELEPIQGPRG*GDCPTPSQS A*GGVLSCTPESHTF*KKPPPTGGRRWA RLGLNGAT*GREEPLQTRLPAEYPGPGP IDPLQPPP ISTASMAFSDFLLLGRDP A
13136	27037	A	13276	865	667	KFLCILDLFFFI*EMRSQHRLECSA IIAHCSLKLASTDPPTSAS* IAGFTGM CHCAQLFLTF
13137	27038	A	13277	103	375	WSRRLPWRRLGYIELFQGLEIRHHFLF GPHYLRRTOCQGPV*PSELGQGWYMS PGV*DQPGQHDETPSLQKI*KTSSAWWH APVVPAT
13138	27039	A	13278	177	3	QQTGSRASNSHRRPGAVVHASNPNTL GGRGG*NI*SQKFKTSLVNMVKCLYGR V
13139	27040	A	13279	379	372	SR*WVCMAHACDPSILGGQGGRT*AO EFETSLRNMVRPCLCLGNTNIYIYIHTH TYIFIQN
13140	27041	A	13280	83	1184	PPAHAARASPPSYTWLCYEVKIKRGRSN LLWDTGVFRGPVLPKRQSNHRQEVSSWE CRKHISKMSGGGLSTVYFFHRRFQITWF VSWNPCLPCVVKVTKFLAEHPNVTLTIS AARLYYRDRDWRVLLRLHKAGARVKI MDYEGERCGRGQSGMTGRNSLRDGI CNA INYASLHRTLKEILR*GSPSGLIVSLLS PPAHPPEDSPGNESWLCTMEVTKHSA VFRKRGVFRNQVAPKSYLHPK*ELSSWE RRKHNT*HTNYEVTWYTSWSPCECAGE VAEFLARHSNVNLTIFTARLCYFWDTDY QEGCLSLSQEGASVKIMGYKDFVSCWKN

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						FVYSDDPEFKPWKGLQTNFRLLKRRRLREILQ
13141	27042	A	13282	1558	1824	SFPYLASFPFCLGLPLETLFHPGL*KD *SDTHTHTHTHTHSHTHAHFSPFPDP LFQSSPFFSSGFIDEYKYPHLWPVMSVTC CRFCV
13142	27043	A	13283	1	519	PHFFLPQGFWGFSPFPL*KSSSPLKAL IFLGGFSPFPFPPKRRFSKIPRGVFFP PPKGGKFFFPFG*IWPPQGFLLKGPSS SSSSSSSSSSSSSSSSSSSSSS
13143	27044	A	13284	349	159	CPLEPKKNYFFCFF*ETGSCYVA*AGL VLVASSNPPASASQIAGIQGTSRHAQPC RIFLSKT
13144	27045	A	13285	748	869	WLGVAHACNPSSLGGRGGQIV*PQEFETSRGNMARPQSL
13145	27046	A	13286	315	410	VQWFTPVNSALWESEAGGLEIRS*RTTWAT
13146	27047	A	13287	355	499	ARCGMHLYSQIFGRLRWEHCLR*KVLS QVWWHAPVFADIWEVEVGALLERSRL *CAMLLPVNSHGPPPTWAMQ
13147	27048	A	13288	880	701	KSYFSSHLHFEGKKCVSSILD*STLVLM CSWLMNYTHHTYIYIYTRTHICVHVYV HNF
13148	27049	A	13289	379	434	KRGPPPPKKRGCFSEKFF*GPPKTPFF FFFPKKKKKKKKKKKKKKKKGGRSRS RLADAWADAW
13149	27050	A	13290	253	344	GLFYNLQKIKIFYVKNLFFFFSNSITEA GVQWPNLGLSLQPPSPGSDSPASE*RIV V
13150	27051	A	13291	561	745	AWEPSLVGETNVNSFNQKYNWPGAVAH TYNAGTLGGQGGWIT*QGEFETTLANMV KPSPY
13151	27052	A	13292	289	2	TLPQGEDFNKFVFGSIKQLQINL*NTD FIGNVFQSWAQYTPVPPSWVAEVEGS LAARSSRLCTIITPLNSHCSLAWATQQ DPAGRVGRPRV
13152	27053	A	13293	281	229	LKNKNVNKEKLRQGVVAHACNPSTLGGR GGWIT*GEM
13153	27054	A	13294	276	441	GLFPKFLLQKINQNWPDVAVHAYNPSTL GVQGRWIT*GQ*FKTSLANRGRKSENK
13154	27055	A	13295	258	389	NMVEKRLGQAHAYNLSTLRGQGERIT*A WEFETSLGNVVRPCI
13155	27056	A	13296	358	353	SFLAFFNGAFLPLRGFFWKTFFFGGVCW RRPPL*RKKKKKKKKKKKKKKKKKKKE MFKRNIGGEERGGG
13156	27057	A	13297	196	1	LMGKAPFLGGFIPPAPFFFLKKKKGGPG AVAYTCNLSTLGGRGRWIT*QGEFETSL ANIAKPCSC
13157	27058	A	13298	182	436	GVTIILNVRHRHRKKVTLYRDLKKVRKCP KLHGNLRKVFQAEGIASCKTLKGHVWWL MPVIPAL*EAKMEGLLEARSLSAWATQ
13158	27059	A	13299	334	440	RHYWLN*AFYHSSLAAPQGGGHWPFP GITPLNSLHVPLLNLSA*LASGV*LT*A HHRVLPNNRALIIQALRITRILGLYSTL LPA*KNFAPFTISDGVYGSFAFF*ATGC HGLNVIIGSTFLTICFIRQLIFHCTSKQ *LWLEPPAWDW
13159	27060	A	13300	359	372	KKKKICGGKKNPPNKKKVKPRGEKTPLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GV*PFFCLEGGFFSPHKFFFFFIFSPNIC SPKKSFFLKFPFPALFFFNLPFLKNIPSP PFLKKASF*EIFFCGPPPPFFFFQNTLF FFPPPPPPPPPPPPPPPPFLDKFAVY
13160	27061	A	13301	233	406	VTVEGMEEVLASSEGMSRPTS*V*FL KYL LGAVAHAKPSTLGGRGGRIT*AQE LKTSLCNKVRPRLYKINK
13161	27062	A	13302	92	429	GSHFNSELIEMKFYIIRNIFITLNCFY LIKHHQHFHYTKFLLVSVINKF*LATVAH AYNLNTLGGQGGRSA*THEFKTSLGNTV RSCLYKNLKMSSVWWCTAIWEAEVRGLP
13162	27063	A	13303	302	140	GGAVNSVQSQAWWHMPVVPVWEAETGL LKPRSLSL*CPMIVHVNSHCTPAWAT
13163	27064	A	13304	115	312	LRSPSFVLSRLKCGGTIMVHCSFDLLG *RNPPALPSKVETIGLHHHALLRLIF FF*KWVVLFF
13164	27065	A	13305	90	246	PGVVAHACNPSTLGGRGGRIT*GQEFKS SLCKIAPPPERKEGRKEGKKKKERG
13165	27066	A	13306	19	310	DSSFSPIMCFGMSVNKTGLWLGGKKKKK KKKKGGPP*KKPLGGPNLPGGGKKKFFP *RGAKKNPPGDFWKKTLFLGGEKLGPPP PQK*NPFFGGGKIGPTPPPKIKPFGEKK KF
13166	27067	A	13307	179	56	WVLVYKKQSILG*AQWVMSVISALWEAE AGGSLVSTSLRLA
13167	27068	A	13308	425	290	KKNIYLAPPGYFWPPQRFLLSPPPPPNV VIFFFFLFFFLFFFLFFFLIQAEGIG VMRGRGEGKMGW*W*KFGRRVLNIRSI LLANFKHVVPYW
13168	27069	A	13309	214	371	IYF*RWISQAWWLMFPVLPKLWEAEAGG *LEPMSLPGQYNETSPL
13169	27070	A	13310	975	572	AWGMVVGVGKHSLSVLGIEBCASTALS LDKSGWEEAARREDVLCEDRRCLLCHV PAGVRGSLKPELGSRKGNGQQSGSKPS VPSLGPRPQGPNGPALSKGTRPN*AICF LCQTPADHSACKQAPHTLPIR
13170	27071	A	13311	270	10	TPNKSLI*RLQFSNLIKLANLGLGTMHS CNLNTLGGQGARITSGEEFKTGLGNIDP IPIESKVIKTLAGMVSPDAWDAIKRTG TSG
13171	27072	A	13312	103	290	LTEVVGVL*NCIYLLPQYTSTRVHAY IHTYIHTHTHTSGLSSTSVGSTNHKSKI FGGKKG
13172	27073	A	13313	136	1	SNTSSSLVTQAGGQWCELGSL*PLPPKF KRFSCLSLSPSSWDYRRL
13173	27074	A	13314	88	183	RVSTLLKKSCFFFFFFFFFFFFFFFFFFFF FFFFSSQKKKNLKNKKRE*KKSCFFFFF FFFFFFFFFFFFFFFFFFFF
13174	27075	A	13315	481	517	LLSP*RPKGKPKGKKRPNLKEKKIGEA RGGKERQRKTPORTGKQKKRRKYRIRGR RNYR
13175	27076	A	13316	307	196	GMHLYLPRTW*WVRVIPSREIEVHAPL EPGSQRLVAEMTPMHSSLDNMNKSPPF QPPKTEKQTKNPPKPHIA
13176	27077	A	13317	2	209	PARALDLKSPYMESCSDAQAGVQDSIY GDHL*LRAPAV**GQTVFVASPSKVGGI TGASHHPGLFFLF
13177	27078	A	13318	3	178	SFCFVSLREIIGQSLIMKTLP*ITHHT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						HTHTHTHTHTQREIERERDRERGESQVLGC
13178	27079	A	13319	40	382	DSVPSLLLLKLLMETGPHHVQASTTTTPS *FFTLLEGFHHVAHAGLKLPSSSRRPPLHA SQSAGIYGCEPLRSARLIINYIGSRLWG LRNICLSQDHEECLLCFILQAISMYRFC LG
13179	27080	A	13320	107	1	PPLIMANSQWAWLTPVVPPTLWEAKAGG *SEVRSS
13180	27081	A	13321	111	382	ASSQLLELAIQVFPGIWIPPTTKQKGVP SGKTLVTSKIIAGLKMPKDSRSRPRTVA HTYNSSTLRGQDRRIT*AQEFKTSLGKI GRPCLF
13181	27082	A	13322	49	108	CGLY*FFF*ATRSWHVAQAGLEFLGLSS FPASASSVAGTTGMCHHTQLHY*F*V
13182	27083	A	13323	1	257	ARGERERERERERERERERERERERERE RERERERERERERERERERERERERERE RERARERE*ECV*EGETVSDRERDFERA PPRVLGAVAIYIEVVCLASLIQ
13183	27084	A	13324	1	248	EFQYILCSALIFGRSKILK*ATKEVKKS KHIPRISCQDTRKYNWSAKARRNTTGT GRMRHLKIVYRRFRHGLHEENLFLKH
13184	27085	A	13326	375	1	PPKRRGKTHCSPKVFPPQNN*TTTTPP QLIICYL*RGGVFFSLPLII*APPAFFF FFQFFFFFFFFFFFFFFFFLQGQYWQFRDT DAEGHLASSRPSGAVFPSQGMHTTGSTR RWGQCVFPPTRP
13185	27086	A	13327	382	15	NWPKNCPLHFQNWFLRKTPQIFFCLKNF FFFFPKKVFYPPKKPFLEKPWPVPLN*K KPPPPFFFGWGPQYCPFKAPPLFI RGKERFPLWGKGDFFQIPCPGGLKKKK RAARDLGTS
13186	27087	A	13328	2	220	GRVGSSRAVALFFFFFFFFCFFFFFFF QNPLPKRGEKKNTPLKKRPLRGGFK KQKEC*EKKKKLSGPK
13187	27088	A	13329	427	289	IQLWSSL*K*LHTHTHTHTHTNTCTFI TVMKELSTHPGNK
13188	27089	A	13330	203	269	INFGPPREPGGFNQKPQFPSPAGFEPWN PPQGPKP*KKKRRKKPFKWAPGGGSKV QNPGLRETGVFG
13189	27090	A	13331	216	418	DVPVHYCRLYKPTLRLHSIYKKQILW PGAVAHACNPITLGGRLWIT*GQFEA SLANVVKPHLY
13190	27091	A	13332	160	325	WERQLFKIAQSGLARWLTPVIPALWEAB EGGLFEYTSRL*LATQQDPISTKMPK
13191	27092	A	13333	339	62	GMLPLFVPPQKRGSPPYPCYGVYNSPPL KKQRFSSSLGIVLPPIVFITPPPPAFF FFFCFFFFFFFFFFFFFLI*RRLMRMRM FSCFLHCP
13192	27093	A	13334	45	384	DPSVRINTLLALLLIRITF*LPQLNGYI EKSTPYECGFDPISPARVPFSIKFFLGA ITFLLFDLEIALLLPLP*ALQTTNLP LGMASLLLIILALSLEY*LQKGLH*AE
13193	27094	A	13335	270	660	AGSRRPLRVPGFSLSMSPSLCRPVCVA QCIRVSFLLTVGAVLRPGFQCLDWPCLV YARLSGWTGFPFCRYGKGCRCRYDEGCC RFGEGCCRCDDRCRCGEGCCRCDDGCC RDEG*CRDDGCCHYGE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13194	27095	A	13336	298	349	KTPFFYGLRGSKIGTL*CSGVIIAH*SLKLLGSSDPLSLVAQAARTTGACHHDQLTNAFFFFPLERVPTPLKNNPFLWVKGVKNWDL
13195	27096	A	13337	865	518	KSATMRMVEDTHKMPAWGGYSGSLQQERGELSSLP*PESPPPLLIIFLKLPSNPLPCSPLPCTQGPGQAPAPVSIHTSLKFPNAKLSVCLSRATIEFS
13196	27097	A	13338	154	354	FNLQVKPDGYFVLFICHILPTDSKSGKAPGAPCHSRNFHIRKTLGWVQWLTPVILALWET*FSHQENSGLGAVAHTCNPSTLGNQGGWIA
13197	27098	A	13339	262	11	QHFHSRKLTP*KM*LSAHSNSTHEAYVAFPKAHKPGLNSTAF*LGTEAHACNPNI LGGQGGQITRGQAFKTSANMAKPRLY
13198	27099	A	13340	358	164	TKKGKPRFFLKNSKISRWWWAPVISGPWEGEGGAFV*TGRPKIWLTEVGPLPFPNLGKKKENPF
13199	27100	A	13341	147	2	FRPQKVSVRVGVLAHACNPITLGAQGGHII*GQEF*ASMANMVKPSSC
13200	27101	A	13342	367	17	TSRSWNLFHVLVRFPPTADKDIREIGSFTKKRSLIDLTPYAWASFTLMMEGKKEQVTSSINGSRQKVRSSQSGELSLTPSDPSWAHWLMPVFPALW*SETGSLFEVRPSRPAWPTW
13201	27102	A	13343	166	492	EGTQETLCGCIICLVRGDALNLFHLKCSWVGWRGAICCMELRETAKQLSVWKLYPEIVFSFSNNNPRPGAVAHICNPNTLGG*GCRIARAQEFETNLCNIVRPHLFR
13202	27103	A	13344	804	1124	TFFFCFFL*DRVVDVAPGWESSDMTMGPLQALTSWGSTDPTTLGLQSGLDLQDTWPPYPTSFYFFFLQGRGTLMLPRLVLNSCTOAILPPQPGQRSKTPISLKTN
13203	27104	A	13345	280	448	GGGGKKKKTTPKPPLEKNFSPPP*FPPP KKQIKPPPP*GGGGKKKTPKPPLEKN NFSPPPFKPRKGIFFLPPLSWVKKKGDPGGTRPLAPL
13204	27105	A	13346	232	400	AELLRYCSCGHFL*SMARYKTKPGVRWLTPIVIVFWAEAR*LHEPRSSRPASATQ
13205	27106	A	13347	138	332	RAVVKPSFEIFYFFF*RAHTF**SCVCLCVCVCVCV*THTHTHTHKHTHDY
13206	27107	A	13348	314	395	WLGIVAHAYNPSTLGT*GGWIT*GPEV
13207	27108	A	13349	388	371	IMNGWQDKELVSRVIQTGIKK*KPRNRP EFRAPP*WHERNGRKERERMGRKERER KKGKGERKRKKEACIYKVKIEISNNLANLI INVER*DRRRPDILSWVLSRVS VFIALVTCLTSPQFFLSLHLNQLFPLGKNL
13208	27109	A	13350	412	40	LVFRFWMCLFSRELFGCFSHLLTKSMSQM*VVAFGDIMYTFDLLFIKKTNNCKLWQGCKEESLIHCWRECKLVQPL*RPI*RS LKKLQMG LYPDPAISLLETYPKERKSVY*RNICTSGRVG
13209	27110	A	13351	372	148	FFFFFFFFFFFFFFFFFATGSCRVA*P GVKWLIISTVPLLIISTGVLTCSISDLGQPVHTSLGNLVVPYSQELPY
13210	27111	A	13352	209	206	KKKKKNFFSFHGKNPNGGPFPGPPPPPF*TFKKGGGLPKGPPPKGFFWNPPQNG

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						GGGP*PGGEKKT PKPSLGLV L F F F F F K F F KKRPTA F F F L K K K I F F
13211	27112	A	13353	43	334	KKKKKKKKKKKKKKKKRGGGPFKISG GAQFFRGEKK F F F F L G G G K K T P R G F F E KKPFFWGGNFW P P P P Q K N F P F G E K K K F L GGGGGKNRV F F W G E K I F S L G F F L K K F F * KKPEGKN F F P P K N P V F S P P P P * K F F F F PKGEI F L G G G P K I P P P K R F F F K K P P G G F F S P P * K K K K F F L P P E K L G P P R N F Y K R P P P P F F F F F F F F F F F F F F F F F F F
13212	27113	A	13354	264	496	KPTILRVTHFLEGCEKYEFLLPVAFSNF SEPLKRYYYWLGAEAHVCNPSTLEGRGG QIT*GQEFETSLVN MV T C L Y
13213	27114	A	13355	183	9	IRSPKIPEIRV F F F F S R W S Y A L V A Q V G V Q WGNLS* M H P P R A R F Q P L S S L S V P S T * K Y R
13214	27115	A	13356	208	378	EICLEFKI IDEMDKCGKLWLGTGAHT*N PITLGGQGGQTT*GRAFETSLDIMEKRY L
13215	27116	A	13357	256	341	KGQTQWLTPVIPTLWEA*AGGLLESRSS
13216	27117	A	13358	78	344	IVGLFESESKKGQHIVSGWIYLRLLIYR FLFPLFSCLCCK F F F F F S P E T E F C F V P Q AGVQ*HNLG* L K P P P P Q L K Q F S C L T L P S SWNYR
13217	27118	A	13359	259	291	AQ*LMPVVPALYEA E A G G S S L E P R S L L S VWAT
13218	27119	A	13360	448	121	RLFDLGNKKTSSFVQNSENAKYEDSLQF YCRIYIYVYIYVYICIHCVYM*TYMCM YICIMYTYTHVYTHVYMCIH TY M C I * A YICVYIYIF*KACLPLALSTLSSGH
13219	27120	A	13361	125	262	FSFQASVEFTSKTVWSVQWLTPPIISTT *EAQAGGSLEARN SR P D
13220	27121	A	13362	362	46	ARAKGPKKIGFSGKMGP*GAPPPKMGK KI*ITPPPKFL F F F L G K T K I K N P P W G F W PFGFPKKKRGGGARR*KTPSPFREKPPP QKLKRFKTPFPPL F F F F K N P R P
13221	27122	A	13363	378	48	FKKAAREKVSTRKFRGFVCLFWDFFWRQ SHSVTQAGVQ*CDLNLHPPGSSDSPAAA SQVAWTTGTHHTQLIFIFIFCRNKISP SLLKKYKKNLPGVVAGACNP SH L G G
13222	27123	A	13364	174	396	SLIFILEKRECYPRSLFTVANFTVAKR *QTLNCPSTDKWINKMCHITVEYYS DI KRNEIPMRATCRQTLKA
13223	27124	A	13365	76	280	PLLPFKAWQVVGCHYV*KL D * I N C Y F R ALLAFSEYMYIYIYIRTH T H T * I Y I Y I Y IYKLTYSHLKVG
13224	27125	A	13366	133	324	YLL*ILVYCSHLIFSLLCLEGIILWVFI IATLITLNTSHLLINIVPIAILDLAAGQ AAVGLALLVSKKKKKGPPLKKPPLGAQI SPANQRKKFPKPKKPIKTRRGTF
13225	27126	A	13367	488	190	FSYAACFLPQC F V F V C T F I Y L H A D G F L L L I I F F E N S V F I L C H S C W F C F L L Q W F L L M N L F S L F L L M L M H P V S * M E C S I Y S F S S L I I F H F S L M L L F F C F M I
13226	27127	A	13368	229	372	YYATKDFSRPRAVAHTCNPSTLGGRRGQ IT*GRQFETSLANVVKPQLY
13227	27128	A	13369	122	2	KEECVGS GT W W V M P V I P A L * E A E G R G S L EPRSLRPAWTKK

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13228	27129	A	13370	43	412	RPTRPKRQNYGDSENISGCGGLGKKGMN GKSTEDFEGETTLYDAITVGTCHNKFI RSHIVYNTKSGP*HKLWTWGGHDVSV*V PQLRKTYHPGERCL**GRLSMYRGREYI GNLCIFCSLLL
13229	27130	A	13371	136	1	KSPTWPGAMAHTCNLSTLEGQGGWIT*G QGFETSLANMVKPSDAW
13230	27131	A	13372	228	385	GLLIHKLEFKHFWLGTVAHTCNPSTLGG QGRHIT*GQGFETSLANMAEPCLY
13231	27132	A	13373	277	429	LETTTKAGLEPTIIFTSSQMSIWFQNK PWDSSKLFNLLSISSP**SSKNY*PWQS TVAHTCNPSTLGGQGRWIT*GQFEISL ANMVKPARVGRHVIRGLQVS
13232	27133	A	13374	194	3	NQENYIYIYTHTHTYTHYIYIL*LLLQ WVYLAYFLCLSYPSLFAQGFTHTTYTHT HMHTLIL
13233	27134	A	13375	377	228	DRVLLLLPRLECRGIIMAHCRPLRLVSN S*APALSFQSAESTGVNPVPS
13234	27135	A	13376	255	465	NAWKCPFIYKITFVIFLIHVSCKKFRNY RQREWKLPTRPLSPS*AIIFPVTCTYT SRWPEATKDPQKK
13235	27136	A	13377	336	38	VWCTPVVPATQEAEVGGSLESGRRLRQ *AVITLVNEHRESALASRRGPEETSSVK PELPTILAHTCFSLPRTGQDITSRFLAQ RNTENLELQMEARA
13236	27137	A	13378	376	293	FFFFFFFFFYFFFFK*KFLTKKKILSSQ YI
13237	27138	A	13379	215	16	HLTWSFTTATEGSKTVTQHSVYRKAKLG LGAVTHTCNPSTLGGGRWIT*GQYKGI PPHGLEDVQ
13238	27139	A	13380	184	64	VDESLEGWMMDEWMSGWRGGCINRYMHA WMDG*GDGWIGG
13239	27140	A	13381	233	417	LKPITKGRKPRGFFLPFKPKQKKYFWGF KKKKKKKKKKKKKKKKKASRAPF*KKG PQKTP
13240	27141	A	13382	34	360	RWNTTNADHDLKDNILSPPQINLYIRON SSRLCRHH*QMSKSPVKIPAGFVLYI* IYRYTHTHTHTHTHDSELYMETHTRMA NTIVRKNSLEHSYYLMLRMTIKLP
13241	27142	A	13383	214	71	QTLNTDSGPGVVIHACNPSNLGGHGGKI I*GQGFETSLANMVKRCLY
13242	27143	A	13384	352	312	DKQLTLHRTDSLYIFYTY*PPQSCPEIS YNNFPCLSQYLYLCPSLHTHTHTHTH THTHTHTHTHSVGRSLFFSGPHTE APRSRVSVYT
13243	27144	A	13385	393	271	IEGQIQYTSITGNKFKDFYLILCKEGIM SREISPPSSCHLRQQ*RVRLRERDRERK RQRERQRE*GRSVLHPHVT
13244	27145	A	13386	180	440	PVEERTLCEDILCFPSVLLCIQPHLLI QHACFKYPNPNSRFGSWPGAHAHCNPS TLGGGGRWIT*NQEFEARLSNMVKPRLY KNI
13245	27146	A	13387	190	47	EGEKGVPSTILKMETLLGTVAYPCHPST LGGQGGRIAEAEQEF*DHLE
13246	27147	A	13388	188	470	ARPPCKGRDSSAEGPPGPPFSWSSLGC WTREPPGRGEPIQAVRREESAQDWARP ELIIKEWWPGLVAHTCNPSTLGGRGWI A*A*EFENSQ

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13247	27148	A	13389	454	367	NKKKKPPPRPF*PPPPPLGKTPFFKKKNP NPPRGGGNSPGSPSFGGKGKDPDPGGF FPPPPYPRGEGGNPFFKKKKKKKRSLD P*WSSQPCPAYEKELNFAPVLATVTLPP GHSS
13248	27149	A	13390	34	354	HTLLALLLIITF*LPQLNGYIEKSTPY ECGFDPISPARVPFSIKFFLVAITFLLF ELEIALLLPLP*ALQTTNLPILVMSLL LIILALSLEYE*LQKGLD*TEY
13249	27150	A	13391	1089	792	THGFGPQVGSPLDLKQPKAMPGRPSLG NPPPGCQQHSHGAGGP*VPPGPRQPVMA SRNLCPLALPRTTHPPSPGQTRDKPRTQ DRSCWRDPRNGPGV
13250	27151	A	13392	299	428	WIRCGRGRSCLPVPHSAPALLSPLVVD GTRRREAGGGTCQGGSGCMGAHWLGGG EGSGCRSQALPREAAEARREFKHGIPR H*LTESLVSVEFRHA
13251	27152	A	13393	382	413	HGKTHLYKKFKNKKFKATMPA*WLTPI PTLQEAEEASLKPSSRPAAVWTQDPS LQKI
13252	27153	A	13394	64	401	GGIPKEDSQAGFTGIGERQQGLVPLL KNGQLSTDACVPPWGRVGVVERAGPPNQ AGEGGGQQEQCSLGLLPEANRCHPCNPS TLGGRSGQIA*GQEFETSLGNTVRSCPY
13253	27154	A	13395	146	18	FSPGVVAHACNPSTLGGQGGQIT*GQAF KTSANLTVKPKRPQ
13254	27155	A	13396	1056	679	DIQVPERPL*NVPEPEAKGEPDRAVGE HIDRDCRSDPAQQRKIFTNKCRAGCR QREMMKLTCECSRNFCKHRHPLDHD SGEGHPTSRAGLAISRAQAVASTSTVP SPSQTMPSTSPSR
13255	27156	A	13397	440	423	IHSPTQRRV*QRERERERERERERERH ALAERNRTREGISGTTGERGNLMLVGGH LPGPLSSRRLGFCPDGFGGQHCLAQGDQ VRL
13256	27157	A	13398	2	256	IETLGSVEFIPYENTYQTYLKKKNRNS HMQSQPNRKGHIRLKYIAAWA*WLTPI PALWEAEAGRSLESRSRNPVSTKKKIQK
13257	27158	A	13399	102	922	LSFFLFSETGSCSVAQPEVQWCNHS LP*TPGGPSMQFQLPQEQGQRTAVWHGGR A
13258	27159	A	13400	198	55	KDYSAVVHTCNPSTLGGGGGWIT*GQEL KTSQANMVKPHLYKNPKIEF
13259	27160	A	13401	19	447	ESALNLPAGIIGVSHRTQPIFCILNAL ALGVLILERSPLQSPQVPPSHSTKPGS LPSVTPGRGPRPRAAEPTAQGRYNSN PVLISPGSVHPASFALPAEPP*TGAPST PRPCVLRPLLLGNAMDLLCTKLSSRLPP YRT
13260	27161	A	13402	93	410	DSNLNYSLFFHGEADLGTNQVLTHPSTT AMYFEHYCQPP*IVHGTINT*PPVVKHN PIHITPSPCLRASTAINLLSHINCYS *ATPHPLGYQQTYLPLTVHST
13261	27162	A	13403	55	387	SNSHTYSLKKSAGITKFNQNHIVNCICI CQVVVPLEMVNRHTVILCQYPVKPRILY QHHTAILVTILTFTLRPGVVSHACNPST LGGQGGRIT*AEQFKISLGNIVRPCLY
13262	27163	A	13404	39	365	SGDRRVRLLLKIITF*LSQLNGYIEKST

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						RYECGFDPISPARVPFSIKFFLAAITFL LFDLEIALLLPLP*ALQTTNLP LIGMSS LLLIILALSLAYE*LQKGLD*AE
13263	27164	A	13405	32	350	HEFATSTSEMTKGT*IVKRRIKHTLCLC RRCGSKAYHLQKSTCGKCGYPKRKRKY NWSATAKRRNTGTGRMRHLKIVYRRFR HGFREGTTPPKRAAVAASSSS
13264	27165	A	13406	326	668	LQFKIFCMPGIFTTISEVSSMSN*RTAYG SQSFHKIVLI*LATFGQALSC*IL*IHL CYLKNKTKHRALVAHACNPNTLGSPPGR IA*QGEFETSLGSI VRLLLSTKNLKKKK NM
13265	27166	A	13407	170	472	KLISVWSEESSYCVHEGPEVVPQKEYS WLEIGKAEMERSTLESLLGATLEALSSN PTRKMQLGLKLKLQASAFKEEPWLGVVA HACNPSTLGG*GGRIA
13266	27167	A	13408	178	422	FYNRYF*YTKYQTENIVCKIMSFRLLV *KI*SLPGAMAHACNPSTLGGRRGRII* GREFETRNS
13267	27168	A	13409	274	444	LFSQYIVFVHYSSFVLILFV**LFSQYI VFVHYSSFVLILFVILHNYTYIYIHTHT HTYTLIFLLIFSQISLGMKLIL
13268	27169	A	13410	205	23	KEFLKFHRKCICQOVKKIWPRAVAHACN PSTLGGQGKRIT*QGELETSLANVEKPH FSNS
13269	27170	A	13411	25	426	SVWWSLETRSSRLRLKKI*NLQNKRR KFEHRHAQRKYDLETQGEDAIYKLRER RKEEE*EKEEKKRRRRKEKEKKKKPTL LCLKKQRNQHLDLRLPASRTVKKLISVV *ATHSVVPCYGSPSKLIQOSIH
13270	27171	A	13412	227	52	EIGSHSCHPGWSTVAQS*LTLSNS*TQ LILPPQPPRELHYNCPVPCPAFCRQAL MF
13271	27172	A	13413	345	67	SKCCYVVAHDCILLDLICLYFLELVGCV DCFSSSLGHY*PLFV*IFFLSPSLLFWY SHYEHICVPHFSKAPFIPLHFFPSPBFP FLCIEMVYV
13272	27173	A	13414	345	33	KVFFFLIICKMRMKNQKNKHGICLLNS AMNTCISFPLRQIMTTWWLEVTQIWGV LFYLFHFHFIEMGSCPGWSAVA*SQPSATP VWSQVILLPQPPEDLGNS
13273	27174	A	13415	187	415	FNQGWAFLEFFCVIFSYPWKDRNRTIFS IKITSFQESVLKLFCEFEVS*ILKIGLG QVRWLTPVIPALRRRQADH
13274	27175	A	13416	143	50	CMKLQSSI VMLGVVAHACNPSTLGGQGG WIT*GQGGWIT
13275	27176	A	13417	170	17	KQMRKEGNGLLTISKVWKQPKSPSQS* *IKKM*YICTMECYSALRPEFPE
13276	27177	A	13418	7	163	IK*IWYI*TMYYSAMKRKKIMSSAAIW MKLEAILGEVMQEWKTNLMFSFISGS
13277	27178	A	13419	901	709	SGRKTSLGNIARSCLYTKSFKIHCLPVV PATQAEAGGSLKPRSLRLQ*ARSHHCS PVWVTTRP
13278	27179	A	13420	236	4	VIRAKTGSNSLFPFHTFFFGKNLCFF QKKKKKKIYIQSKPGAMAHACNPSTLGG QIT*DQEFETSLATMVKNPLY
13279	27180	A	13421	46	141	NSVISAHCNLCPLGSSDSPSSASRVAGI TGWC*HCNLCPLGSSDSPSSASRVAGIT

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						GWC
13280	27181	A	13422	604	1121	LGSGDLP*EINPLSSCSLLREKDPPTTS GPQTDQPKKHLTNFKSAPYKTITDAELR VTLTVEAHLHPGEINSHVAHTKPVWWSL HTDAHEIWCRRSDCLKLVPTLPLIPLEAA LRNITHSLSI PPPKNFRPNTSTLFCVI FLINIRRQEQASEPKPSHRIPCDLHVY AQMA
13281	27182	A	13423	214	22	IRESSSTPSSPTLPESCNSIPFPF*KFI WSGVVAHAYNLNTLGG*GRKIARAQEFB NSTRAGLW
13282	27183	A	13424	397	330	SEYNSECS*VQWHTLVVSATQEAEAGGS LEARSSRLCALIIPVNCHCTPAWAFPM
13283	27184	A	13425	729	885	AKCYPVRNLSLWPGAVAHACNPSTLGGQ GGRIT*GOEFRTSLANMVKPHLY
13284	27185	A	13426	231	2	ASVFFKATLVDLHW*YIYTYIYTYIHI YTHTYTHIYIYIHTYIYLVNQNQYICLYV HINANQQGYIYTGRTPICFF
13285	27186	A	13427	184	171	LS*YIYIYTHTHTHTHTYIYIYTYE QPSSQSS
13286	27187	A	13428	372	166	CKFRPRKINTTFSHICGS*KVDIIEAA* HWLGTVAHACNPSTLGGQGRWTI*VWEF KASLANLLTPLLQ
13287	27188	A	13429	391	437	MYSLGVGFFHSTI*LLKDIWFGVVAHT CNPSTL*GQDGRIT*GRKLETRPGNRAK LYLYKKNSN
13288	27189	A	13430	39	254	EFIPRAQDLETSQGNVRPRLYRKFKNN *VWWCASVVPAMWEAEAGGLSEPGRLRL HSNMDNGERSCLKKK
13289	27190	A	13431	336	488	DIWPGMVAHACNPSTLGGQGGRIA*A*E FETSLSNMARPWLKKKLARHSGA
13290	27191	A	13432	154	481	FFFFFFFFQKNGFFF*KGIFFFFKLEGR GAIFV*PNLTLP*GKSEAPL*KGKK GGAPPP*LIFFFLKKKLPLLGQGLKL RALGKPPFPFSQGGINGVKTTPFGL
13291	27192	A	13433	388	280	KSKLKGCCVALCLGLI*SVLLA*PKT *LFCVSLDMYIDTTCSLISISYLSIYLS IYLSIYLSIV*SVS
13292	27193	A	13434	187	48	SISSTKGPVAVAHAYNPNTWGGGGGRIT *GQEFETSLANMVKPRNS
13293	27194	A	13435	71	309	DSVSEEEEEEEVELAHPLAERYHCERA ET*VKALLWLELCDERVSSRSHTEDCT EELFDLHARDHCVDHKLFSNLK
13294	27195	A	13436	18	375	RPAVPGRPTRPINTLLGLLIIITF*LP QLSGYIEKSTPYECGFDPIPARVPFSI KFCLLAMTFLLFDLEIALLLPLP*ALQT TNLPLIVMASLLLLIIILALSLAYE*LQK GLD*AE
13295	27196	A	13437	373	27	THPYYSHQEQSP*PLTGALSALLMTSG LAM*FHFHSITLLILGLLNTLTLYQ*W RDVTRESTYQGHHTPPVQKGLRYGIILF ITSEVFFAGFF*AFDHSSLAPTPQLGG HWPPTGITPLNPLEVPLNNTSVLLASGV SIT*AHDP
13296	27197	A	13438	575	699	LGTVAHTCNSSSLGGRGGWIT*GQEFET SLANMVKTCPOKK
13297	27198	A	13439	247	168	LENLIYTRVLERHREAKVHFPFSNISYS DKRTDTFVLTKTH*HTHTHTHTHTHT

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						HTRGSHFFY*HTHTHTHTHTHTHTTRGSHFFY
13298	27199	A	13440	391	168	TKKKKHPSPRGAREVFF*QPPPPFCVL*FFIVFFLSQGGGGGGGEFFPPFPPTSPSPPPRGVWKKTPPFS
13299	27200	A	13441	403	246	LFPTAIIGGPPGFPPPPF*NEAPEFFFWGPKKKKLSPPPAIKMVFFKGPPP
13300	27201	A	13442	305	414	KNNFHPSTLGG*GGWIT*GQALETTS LGNMVKPHIY
13301	27202	A	13443	269	409	PGTVAHAYNLSTLEG*GTMITQGQEF*I SLVNTVIPHLYQKKKKGR
13302	27203	A	13444	295	37	DPSYLAWHMVTTPHQVSTQHTLPRPRPCLPEMNFLVSLKIWQCWPGTVAHACNPSTLRGRGGWIT*GQEFETSLANMTKTRTRGSAR
13303	27204	A	13445	256	388	FCGFWPGAEAHACCPCTLGGRGGWIT*GQKERTSLAHMVKPRVC
13304	27205	A	13446	277	374	SRLTATSSRGGWIT*GQEFVTTLANMVKPLLY
13305	27206	A	13447	14	387	PQVIHSPWPPKVLGLQA*TTSQAWLTPVIPALWEAKANGSLEVRSS
13306	27207	A	13448	185	379	HFGRPRPADHLRPGATNHPGPQGETPSL L*NTKKKKRGRPFKKKKLQSLVWQNKIFFLAELKLLW
13307	27208	A	13449	168	346	ISILRTNNMISIKINLRLFIDELKKRDPFIFPYFFFFFFFFFGGNHSL*SLIVIFLIC
13308	27209	A	13450	57	176	VAESRPGPGGTATELVPPSTRLLTRAPRDLLTGKRKPPPLGRMSRARVQWHNHFTESCSVAQARVQQRNLGSL*TLPPKIKQF SCLSLSSWEDCLSQRVRDCSEK
13309	27210	A	13451	411	241	PPLFFFFFFFFKQKFPSPV*GGGQGWDFGSLQPPPPRVKQIFCPKIPPPWPPKKGVP G
13310	27211	A	13452	307	298	PTHSIVRNKSL*IN*TSSMCSGLKVMRR*SQKQEDP*SGVVAHACNLSTLGRRGWIT*GQEFSTFLCPSA
13311	27212	A	13454	191	108	GWSQTPGLGRSSLLSLPQWWDYRMQCRGVILAPHCGLDLLGSGDPPASASQVAGTA AFENCATSFWLP*FLNTQCFKIYKTKN
13312	27213	A	13455	242	400	IATLLDYLQIPNTGPGAVAHACNPSTLGGQGRWII*GQEFENSLANTVKSCL
13313	27214	A	13456	1	346	YVTTARCSCWAGTESHMGAKDFYRQEKHPFHADSGIGWA*DRLRQRYGRFGRM*F SWARGAGEKHS LA*AQWLMPVVTTFWEVKEGRSLEPRSLRPAWATWRNVSTKIKKK KKG
13314	27215	A	13457	166	289	VRSSKLN TWVRWLVP IILTLWEA*AGGFLEPRISRLVWATQ
13315	27216	A	13458	220	76	TASLKLKSWLDVVAHACNPSTLGPGRWIT*GQEIKTSLANMVKPSP
13316	27217	A	13459	219	46	SPPLKKKNFFPPGVMGAPPRFFLKGPPQNFFFFFFFFFFFFFFFFFLKQ*EQTFLLIY
13317	27218	A	13460	126	1	VVSLGAVARSCSPSTLGVOGG*IT*SQEFETSLANMVRTLTS
13318	27219	A	13461	330	420	NICSWAQWLTPTVPAL*EAEAGGSPEVTSS

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13319	27220	A	13462	577	766	AQWHTSIVLAA*EAAAAGLLEPRS*SRLKCTMIIPINSHCTPAWQHMRPCLLKKNFSNSFISK
13320	27221	A	13463	206	387	VTVGETEAEAGRGHLLTCCVLKTQKWLGTVAHAYNPSTLGG*GGRIT*QDEFETSFLGS
13321	27222	A	13464	167	41	DFWLGAVTHACNPNSVGG*GGQIT*GQEFETSLANMVKPNWS
13322	27223	A	13465	480	79	SRVISPLILNSVISAKSLLPVGSQGKSKGQVWSTQEERLEPGVMGEFTPGPCCLVSQGPSLCPSPPPYSFRWSRLSQAPGSI RVLI*RPAAATSAPPAQLGLPDTAFPP PLLSRDQQAAGRQGRDKGLP
13323	27224	A	13466	3	373	DAWVAHASAHASVCLITDILLALLIIITF*LPQLNGYIEESTPYECGLEPISPARVPLYIKFFLVAITFLLLDLRLALLPLP*ALLTTNLPILVMSLLIIILALSLGYE*LRKGLD*AE
13324	27225	A	13467	214	55	TRQKIFNLFSS*KKFLIPPARAKDFLFFIFFFFFFFFFFFFFFFSCSRILLHR
13325	27226	A	13468	111	358	VMKVFI*IGELVTQAYIFVKSHQIAHILFHSMYVLP*IKMFWPGTVAYTYNPSTLGGHRRIS*AQEFETSLGNIVSPHLY
13326	27227	A	13469	199	607	RIRGTSQKLLLLLKLISLIPKSQPTRGTP*TTFPPTNTNFPFPPVAATAPDPSPAHFVSSPYNPDLGSP*PECPSPGRLQREIEQCKKDIONFPPTTSRICSNDSLKGSASRRRGHLFCERPVNQFRSPKPKK
13327	27228	A	13470	128	256	EDWMWWLTPVIPTPQEVVRSLEPRSS ELQ*AVIVPCTPSE
13328	27229	A	13471	94	388	KGEGKTEELWSWRSHRGTHLCLLADISALPLHYYYYYYFWQRWSLPDQPGQHGETPCLPKIQIINRAYWHVPVPTDQEADAR*LPEPNRQRSORPE
13329	27230	A	13472	359	73	ATEPGQLFYF*EESHNVQTAGVQWLDHGSLLQPPPTGLKPSFPLIHTGITAASHYT WLNQLLPMNVSLTTFYESPQLKIQRSHILCNSIHKFLE
13330	27231	A	13473	332	10	ILSKRGFPKPGRYCEVNPFLCVQGA*VRP*EDTSLHCEIYHTHTHTHTHTHTNLKP*TSKELIPQKTESLFFSLCIKKSLLRFQTFPDAGSTGNSVGCACFISK
13331	27232	A	13474	355	385	IMVCIKQSCVH*KNN*FWPGTVARVCNPRTLGGQDRQTA*AQELKTSLDNMAKPCLYKKFF
13332	27233	A	13475	297	425	RKSAWWLMPVVSPL*RAEAGGFLEPGSLRSAWATWGDPHLYKK
13333	27234	A	13476	160	1	KSTGRLGMVAHICIPSTLGSQGGWIA*AQEFETSLGKILSLPEIQKSASLITW
13334	27235	A	13477	334	79	GMKEQINFLYQKRGIKPNKLQAEENVVLIHYN*KLLSNSFK*LQDTAST*YFFGNLYNRPGMVAHACNPSTLGGRGWIT*GQEF L
13335	27236	A	13478	234	385	YAKFHVSINEKKPDVAHACNPGLTGGQGKWIT*GQEFKTSANMTKPRIY
13336	27237	A	13479	408	129	KRSINRKKGGELSSSHFLLLLPPLDEEPPSPPPFCPLPPPPPCPRLPQSG*GACGRLHPC*MDLGPCKCPARKVFSHLSCSL

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						VLQVCRSP
13337	27238	A	13480	251	384	TITPWRGAVAHVCNPSTLGGQSRQMT*GQEFKTSLSNMVKPRLY
13338	27239	A	13481	164	300	AGDDSDNSMGLLGRIHEIKFFKCLGPCM TTKFIVPALWEAEVGGWLEPTSLRLR*ALIALLQCTPA*GTVYDYKVYRPSTLGSRGRRMA
13339	27240	A	13482	2	30	TGCHQFRFLNPFSPHPVLQLVSPGPDCLIFRYFKF*LHQLM*INPNANFCGARSFLCKFRVWIS*LRYPVALSVLFVFK*S VQI*VKKKKKKKKKKKKKKKKKKKK
13340	27241	A	13483	39	199	LDVGTCSPIVPASQEAEGRLHEPTSLRLW*AMIVQLYYSLGDRARPCLYLKK
13341	27242	A	13484	18	72	TRTRSYPGSTGCQLHTFGLVSLYNCSQFLITNLVYISLYRDIY*YIYIYLYREIYLYIYIEIYTYIERVYVIHI*ILGLQVANCEPLD
13342	27243	A	13485	266	496	LDSASDITQAGVQWCNHSFL*PQTPLK*ASTSAS*VAEITGLSQHVWKIIMSVSLSSYTFIQLEPSILLYGNTAP
13343	27244	A	13486	286	72	HILSHCTVLWFLTPHHGTHYKNTTGQPSIVAHATHNLSTLGG*GRWTT*GQEFKTS LANTVKCSDAWVDRD
13344	27245	A	13487	309	6	RFFFFFFPFGKKGVFFQRFFFGFPRGFPPRFFKTGPEIFFFGPLKKKKNFPPGGKIVFF*RGAPFFFFFFFFFLFFFFFFFFLKKNYLLLEKVQSPEKEG
13345	27246	A	13488	183	459	RRVKKICKCIIWQNNYL*KGINICSMPOKKKKKKKKKKKKGAPFKKKKKKIS*GGGPFF*GTKIKPPGGRGFFFFFFFFGEEKIMLFPAVFI
13346	27247	A	13489	348	1	CEBGKGLPIQFASWFKYAGFHSLESIFQSFCQTKKLEAPKELSPCSQLYRYNWQLTCRRMKLDPHLLPYTKINSRPGAAHA*N PSTLGG*GGWII*GQEFETSLTNMGETP PTRP
13347	27248	A	13490	313	320	KQGGPPLAQARVQWYNLSSGETSLPLPGSSNPPPSATGVAGTTGSPPLA*LIFFFL*DRENGDQRKL
13348	27249	A	13491	187	350	GNPVKK*IKNTSSSGWVWMLMPIIPALWDAEVGGLLEPRSLRPWATERDSVS
13349	27250	A	13492	211	83	EYAKKNGKLLSWRKYL*SVVCVCVCTTCVCVCVCVTTCIKNI
13350	27251	A	13493	286	407	LGVEAYACNLNTLGG*GGRIT*GQEFETGLGNTARPCLYF
13351	27252	A	13494	897	1033	KFIFKQMQWDDHSSSLQP*TPELKQSSCLRLPSTWDYRREPLHLAM
13352	27253	A	13495	265	3	HLILLEEELTWQRGKWLKGRVSLCSLGS*TSLSLTVLKKGRGLGVVAVAPSTLGGRGRWVALAQELETS LGNMVKLSLSKIQKLAGMV
13353	27254	A	13496	319	1	CFKLWDTCAQCAGLLHRYTCVMVVCYTHHPEFCYNIMGLPKYMWSYLWPKCCHAVYHFRYIKNLLPGCVAHACNPSTLGGRGWIT*GKEFKRRMKTIV*IGIYFI
13354	27255	A	13497	265	11	VLGEVSNQHLGAPSNRTPSEVPLAQAAQGRPSLVPPSAIVFPSTICYAFSLISMPIIP*VWEAEVGELLEPRSLRQA*ATW

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13355	27256	A	13498	164	22	GIKRRKLIKSGVVAHARNSSSLAGRGGWLT*GQEFETSLAKMMEIPSV
13356	27257	A	13499	277	363	TYLCYIFNICLFVGEIEKQR*LI*FHRS TLNGHILYVRPVPSPNPSQAVASPVTCTY MPTWPEVVESQKK
13357	27258	A	13500	1	270	YTCSVLLLVTVNLLLCILYKLNFTIIGML RKKTVYIYIERIQYYLKFQASTGCLGVY PTV*PYMYTTYMYMYMYIYIYIYIIL CLCLDG
13358	27259	A	13501	170	383	ILYSSKLTYPSPQIVIFFCGKST*GWVW WMPVIPA*EAEVGGSLESTSLGQAWA TGRKAFFVIFYKEYKN
13359	27260	A	13502	31	402	GDYLYLREGWQEPARREQAQNLEPNRT FPHLICTNYRFLSLAWSECEERNET TDKNQTVKDLALDMKRVLPFS*GHQKVI KVGVVAYACNPSTLGGQGQWITRGREFK TSLINMAKPYLY
13360	27261	A	13503	232	446	RNRPGAVAHACNPSTFRGRGGRIMRLGD *RS
13361	27262	A	13504	196	390	VNKAEEKHLYFVARKEILRPGVVVHTCN PSTLGGRGGWII*GQEFETSLPLPKTQK LAECGRGCL
13362	27263	A	13505	146	7	LKYVLYWLGAMAYTCNTSTLGGQGQWIS *GQEFETSLANMVKPCLF
13363	27264	A	13506	177	18	SQNFGRPRQDHFRLDGRHSETPSLQEK VKKLTRHGGACVQSLLERLRREDHLGP GGGGCSVP*SVNII
13364	27265	A	13507	117	338	NKILKKKKGGGRFKESKFTSPGLQGNST FMGPPKLNLRAGV*QRRGKNLGVPLK PFEANPLFARGPNTKNP
13365	27266	A	13508	306	443	LARYEPAVRTRAC*AQWLTAVIPVL*EA EAGGPLEARNLRPAWAT
13366	27267	A	13509	146	390	KMFKGHEQAHRKKKKRGGGRFKGSKFTS ACLQRNIFFLGPPKLNLRAGV*QRGDWK NPGVTQFNRFENPLFARGPNTQKP
13367	27268	A	13510	119	356	NEDRNLRGGCPGR*LLRTEGVCSNPAGW SGIRWCEESGGLFWRVVRGTESVLFSGL FVCCVFAQEKAKATGRAEVS LCP
13368	27269	A	13511	221	21	EDLQDKPLGSCYSTCGWAEQWYLQHPG GAGSKCRIWLGAVAHAYNPSTLGGQGRW IT*GQEF LSL
13369	27270	A	13512	163	418	TFPDDQCLMLQDHACVKRSIQSA*YLTP AVLAHWEAEAGLLEPTSLRPAWAT
13370	27271	A	13513	239	21	FGNLGGPGGRTACIQFSLGNIVRPVYFK TKPKPKPNQNTKIS*AWWCMPIVPATR KAEVGESLEPRRSRLQ
13371	27272	A	13514	135	11	KFFFWPGLAHAYNPSSLGAQGGRIT*G QEYETSLANMVKS
13372	27273	A	13515	162	57	BGTLRSRRPPLGGWVT*GQEFETSPANM VKRCLY
13373	27274	A	13516	424	54	PKRGFFPTFFIWVPPVFLPPFFKPPPR IFFLGGPPKKKFFSPPPGKIFFF*KGPP PFFFFFFFLEFFFKKKKRLGGFFFFFF FWARPFSFLSLFFFKETIPLYNIWMHK DSCKAVIHVYH
13374	27275	A	13517	310	349	GGGPLKKKLFSSRGGERFFFF*GAPFFF FFFFL*SSKIFIFFLKSF FFFFFFFFC FFFFFFSQILFFISSPCFVFFFLNYSRT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CSYVCALILFKGNTYSRKARHILW
13375	27276	A	13518	273	393	IKCLSYRKKATTLGGQGRWIT*SQEFET SLSNM*KPQLY
13376	27277	A	13519	450	139	IPPIALVSPFAKHTWQQMGLVRRSSKG NNMSKGWEIIHPSRIFCSNHTLLRIALW LGAVVHTCNPSTLVGRGGWIT*GWEFKP SKTSMERFCILSRHKRTRGS
13377	27278	A	13520	47	427	KMKQLFEMLVFQNWITIFLSHSIFRTIR* LTLEPLMFRYYFKQ*RTLLPPKF*DRVW LCHAGGCL*CSGTVSAHCNLRLLGSSDP STSAS*VAGTVGAGHHIWLILNNRELPK QKFFINSSRNLFET
13378	27279	A	13521	199	98	SLPSVKLSICCEFPEDIVSKDPIPVVLP VVKRESCLCALPNLLPK*EKTNIQVP* VFQSTIKAKAQLGMVAHACNPSTLGGRG GWIT*GLR
13379	27280	A	13522	314	18	QTLNFYILKIYNIISLVHC*IFEARFQI LV*V**NYPF*SLICFTFSWHETQNT** KNLIIWAGAVAHTCNCNTLGDQGRRIAL AQEIEPSLGNIAIQ
13380	27281	A	13523	18	231	CPPAVFGTSIEQIQLKYDIKD*KIGQAW WCAPVPGTQAEVGGSLERSSRL*CAM STSMNRHCVPAWAT
13381	27282	A	13524	239	465	RVQVSECLHREKCLYFQLGLS*LIPQT GWLKQQKLPGTVAHTCNPGLRGRGKRI T*QGEFETSLANIVKPRLY
13382	27283	A	13525	388	468	SLRLGTVAHTCNPSTLGG*GGWITRSG
13383	27284	A	13526	342	369	CTLNTLLYSISDFGVSAPLATGGDITR NKVRKT*LRLGTVAHTYNPNTLGGQGRR LT*AQEFKNSLSNIGRPHLYKTKTKKT
13384	27285	A	13527	241	231	EYVCIWSHSSLYFSSSLYIHM*VCVCVY IYVHTNSHIYTHMYIHTHTHTHICIYKL EEKYKEL
13385	27286	A	13528	241	231	EYVCIWSHSSLYFSSSLYIHM*VCVCVY IYVHTNSHIYTHMYIHTHTHTHICIYKL EEKYKEL
13386	27287	A	13529	34	299	SAPASASPWGIGVLYRPLACPEDRFSPG PEANCGEIETTELRLVTLSPRLECSGTIT APCSLDLQGSRDPPPSAS*VSETTGASH HAQL
13387	27288	A	13530	158	45	SGHRSRARWL*PVISALWEASAGGSPEI KSLRNRRPG
13388	27289	A	13531	342	1	CFFLKGAPPPFFFFFFNFNFFFLVGTGTD KLILKV'TWKWGPKIDKAVPKNNQARG LP*PDIKIFYKVWLGA VANAYNPSNLGG *GGWIA*E*EFETSLANMTKPQYKYK LA
13389	27290	A	13532	589	742	RIMKMLRIKICGTGPGMVAHAVNPSSLG DGWIT*DQEFKASLANMIKPHLY
13390	27291	A	13533	74	446	HVGIPSRLTSVSHPRCHKHPRTESEHVY CAIEARHYQCKVSRPSDAAGSEGRPRDM TQDTEVADTPPPNISSITATRTMATIGV GVVAHAYNPNTLGGQGRRIA*AQEFKTS LGNLAKPCLYKH
13391	27292	A	13534	1941	1040	AFHLLPYLSSGFYCSLGPCFGLGSSHMA AWHKEPLHNACSDSRRSAPIRQGLGSPS ATHDTHTRTLAHICKEIFKERLHEIKER EIDS*RG*NTQR*VEREEAENKYKPTET

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						NTEIENHKQQEMLRHAGEERENSPREAE RKCNEKCEIKSRNSRKEARLRKKVKFK TNEKGKG*QIITVHKEKREVGRRRGRQ NKKRTKSTQHVTQKGDNR*SVKEEPLLR RAKRNSNKMKNERYVLRQDTHDSCQEKE KMRQRHTRKKLARETWKQVVRHTLNREQR AKPRKKETKEIHIHSAIILKC
13392	27293	A	13535	1192	1476	EIKRKWGPASCHACNPITGRPRRDHL RSGVQGPQGRGETPSLLKNIQISAWAW CAPVI*EIKRKWGPASCHACNPITGRP RRVDHLRSGVQGPQGRGETPSLLKNIQ ISAWAWCAPVIPATWEAEAGGSLETGSG GCTEPRSHHCTQAWVTE
13393	27294	A	13536	55	132	RAESCSLAEDGVQ*GNLSSLQPPPPK
13394	27295	A	13537	7	325	SPVEFRLGEPTKGTSSFGKRRNKTHLTC RRCGSKAYHLQKSTCGK*GYPAKRKRKY NWSAKAKRRNTTGTGRMRHLKIVRTFK HGFREGTTPPKRAAASSSS
13395	27296	A	13538	259	274	KFEAAVCYHCTTSL*CHTVCFLSFFL LEIGYHYITQAQSGAMIAHCSLKLGGSS NPPVPAF*VAETRSACYNAWLVFKFLM GL*ELWKDMS
13396	27297	A	13539	3	68	QASVLPQKQLMSWQKLESTFVKFVNLV KTGRLGEEISCLLVREYYSISDCLATI KLPAHLKSMRKPRHKDFKSTFLISTKNQ GNHGHGTKGNEVNNFQQRISV*KTYFKK YNMRPGAVAHTCNPSTLGG*DWIT*GK NCQNQLS
13397	27298	A	13540	268	468	YRRLISKKFFKRWKSVSFFKFSFFWL EVAHACNPSTLGGQGGKIA*AQEFLTSL GNIVGPCLYKK
13398	27299	A	13541	308	437	FSWAFETGSQAQEVQWHDHLHL*PLPPRF KRFSHLPLSSWDYR
13399	27300	A	13542	7	244	AKTAPLFF*FETVSCFVAQARGQWHD SLQPRPPPGQETSMIKTSSDPPPPASQVA GATGMGHHAKI*FLVETGSPHVSQGG ALLK
13400	27301	A	13543	50	175	ALPAHTAVGQCSVEGFCVLSDEGDGA ARMKLVFLMKLSHETVTIELKNGTQVH GTITGVDVSMNTHLKAVKMTLKNREPVO LETLSILGNNIRYFILPDSLPLDILLAD AEPNVKSMNREAVAG*R*G*AREIFDEI ES
13401	27302	A	13544	47	362	VAFQGLQVPATNPANFFFFWKGFFFP QGGROGEKIGLRDPWPPGVRKIPGPTLS GTREKGAPPPPIYF*FFWKKGGQKGGP GGF*TWDPKGPPSPTPPKGGD
13402	27303	A	13545	97	351	NKKKKGPPPPFF*KKRVGKKKKKGARAGG PPPKPPPGGPRGGPRGQNSKTPRPKG GNPPFKKKKKRNIFPAGPMGLKGGHL
13403	27304	A	13546	214	32	NYIKISSVDGGAKIK*WT*NLKCLVLSV KNITRWVDCSSGVQDQPGQHGETPSLL KTRKTSWA*WRLGLIQRWRKMPWPSR
13404	27305	A	13547	350	159	QTGTLQKTKQKKQAQWLMTVLGL*EA KAGGLLEPKSLRPATWQDPIYKKKFF LERKTWR
13405	27306	A	13548	367	149	FFFFFFFF*TGSHYVAQNWTQIPGLNLP ASASQVTATTGMHHHTRHTPFPSLTST

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						QSVSTASWTYLNQSGRH
13406	27307	A	13549	321	2	GLVKVTHHGVDRLNGYPDSQASVLSFFY TA*MVQ*LQLPDKVQIYPAHPLFINDMP P*WLLKIPSFPGPTVAHPYNPNTLGGRG RRTTRDREFETSLANVVKPHLH
13407	27308	A	13550	216	13	GYSGETVFSMRKQQSGPCLQGPSPIM GKAGINQIIPKTTLGGRGWIA*GQEFK TSLANTVKPCLY
13408	27309	A	13551	199	391	KDFSIFTACFKRPFITGSQQEQWLIFP HAYNPSILGGRGRQIT*GQEFLLPARLG NMVKPCLY
13409	27310	A	13552	70	239	ATCVKN*RTSWAWWCVPVVPATHEAAAG GLLEPRSSRLQCSVIASVERHRTSVWTT
13410	27311	A	13553	105	257	GQAQWLMPIPALWEAFAGGSFAPRSLR LA*ATVPGPNFLKRAFHSLLNLFLLP
13411	27312	A	13554	499	165	Y*MESHFVTQGGQLQWCSLGLQAPPEV GGWLELGRQLPMKPKIPIWTPSPG
13412	27313	A	13555	415	719	YTDKSIIRSISLLPVKGSTHMCVPKFIQ LQEAGGIHMAKLSGQRVDREWRLGTVAH TCNRSHLEGKGGQIT*AVFKTSLGNMA KSCLCCKYQKLSWIWQH
13413	27314	A	13556	224	523	DKVSLCHPGWECGWVQSQLTATISISQG* TILFPQSPE
13414	27315	A	13558	355	1	QVSLQLPYCVLQFQHIYNKQAALLQRCY VSATNLLINAIWQYVNSLKMCEENQNV LQNMPF*HRNYFGEAGHGGSC*SQLLG RLRH*NCLNLGGGGCSELRLRHCTPAWA TKASPS
13415	27316	A	13559	73	259	KYVPHKGKISERRLCSSVAQAGVQWCDHG SRSLEVLGSNDLLASAS*VAGITGCWGS SDPHTT
13416	27317	A	13560	205	21	VVKISEDFLGDAKKWAYQEDIKRLRLG RGAVSHTCNPSTWRGRGWIT*DQEFET SLPKC
13417	27318	A	13561	254	481	LMALLPGSSDVLSEYGWEHFNVLIS KEIFILLFF*DGVSHELLPRLECSGMISA YCHLCLOGSSDRRDLKKQ
13418	27319	A	13562	174	369	TFFSPSMFVEPGPYIAQAGVRWLFTGA IIVHCSLKLALSDSPTSAS*VTATTGM PPLAFTVK
13419	27320	A	13563	371	109	LFSKAGRCILQNLLCCMVSGKCWPMNGI DVTREYPTFAHRVLTAAATSGSDFLGQ AQWLMPIPAI*EANAGESLEPKSLRLA *ATVPGPRSLSQTLHLRSELCL
13420	27321	A	13564	206	486	RQLAAVHILVTPDPDHTWANYVTSLSL LSSSENGVNNDNTHFIGLLRDYK*GWV *WLTPVIPALWEAKVGRIARGQELNSL GSKARPRFV
13421	27322	A	13565	212	398	SRVRGCFPFNLPKSSCI*ECGQGAHA CNPSTLGGRGQIA*AQEFKTSQGNVAK PHLYKI
13422	27323	A	13566	26	395	YSPVHTDKCSGVRKLGLLLLFFFEKEFH FFSPAOKARAKIGLNGTFLSQGKNFRP KPPKKRGKRGAPQPGKILNFKKKRGFS MGAKVNPNGPKGNPPP*PPKGAGKGG TPRPGPFFFFF
13423	27324	A	13567	400	195	ATRVSLAPTCKINWGWPTPIPPPQE GEAGEFL*PQKWRVRLNKIVPLSRPRD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KTRLCFKKKKKN
13424	27325	A	13568	316	154	SQPFPLRWEDRLSRGVNQPKQ*LMPV IPAFSGAEVGGSLPRSSKPA*ATNNLK SKVIIGGQICDKASKVSI VESSWWGWC
13425	27326	A	13569	297	475	FDYFFIY*ETKSHSAAQAGVQ*CKHSSL QP*PPGLKQSLLPWPPKSAGLTGVS YGT WPI
13426	27327	A	13570	116	332	NRVLLLPKGEYRGTTISAHCSLKLIGSKR PPTSAA*GDETTGVCHHTPV*FLKTFF IEIRPGYVPRVGHWR
13427	27328	A	13571	233	405	TVPELRASCRLKKKKKKKKEKNLKKIK GFFPGGPRV*GPEAKNPGGGGPGIPKGP G
13428	27329	A	13572	408	3	TFCDYFKTPPPGKFFFFINGPPSFFLNRG PSFFFFPGFPPFLKNFFFFPLVVKGG GYKRGVFPKKKGPPQPLFFFFFFFLI* KKTRPGTVAHPCNPSTLGGQGRWIT*GQ EFLSSLAKMAGRVVRPGNCESV
13429	27330	A	13573	273	406	IKEFKAERGHS*NTSTFGGQGRWIA*S QEFETSLANMVKPHLY
13430	27331	A	13574	385	38	KKNSPPPPGKNFFFF*GPPSPFFFFF FFFFFFFLGGKKTFFPPPSRFFFFFLPK FPPKNQGPKNFFPPKKKIGD*ARPPPLT GGAKGAPLEFKKKKKKKLKVPRGAVAHT CNS
13431	27332	A	13575	230	53	HWKVLKENKQIFTKISFKMNAIKDSVGQ AQWLMPVIPAL*EPDMGGPVEPKSLRPA WAT
13432	27333	A	13576	406	33	VNSIVWVSSPFRVSTFISFFELKSCSVT QAGV*WHDLSLLQLQTPGLKRS PAPS RG LSFYLLSSIFYPHSSQTELFVGT LNAASF TNSRLLYLSLLLCGYHPLVPSLPLSTI WYFSLRVSHHP
13433	27334	A	13577	426	294	GGFSPFPVFKPPQFFFFGFLKKKISPP PPGEKKIFF*KAPPP
13434	27335	A	13578	268	3	LQAKGPAMGEAGARCSSEVWGWRKGF L*VSR*PSFDSHVRIGRVQLMPVVPVL WETEADISFEPCCSRPAWASWRKTYIQK PQRI
13435	27336	A	13579	395	49	EKKKFFVCFPGFPGNPPNPSPQFF*KGL ISPSGSLRTRRGFFP*RVFFFLKKQFP LSPRVECNGIIPDP*PPFGEVTSTPQVA GAIGPPPPRVNFYFFVKKGFLNVGPMF FFF
13436	27337	A	13580	68	466	GASPAQGSTLHLVILPRYFFKIPTVRTE SFGSLVTSPPPLHFLPLNKERGGPGI P LPCPQLLQVLGGTSLPPVPSLPDTSQDK WPLHGVPPGHVCS*PLAGDGAWPPSPHW IPLNPGTSKSLQAPPPNSA
13437	27338	A	13581	67	249	ATAPGLLC SYKIFSCQLQWCVPTQLAW ETEAGGSLEARSSRL**TMITPVNRHCI LAWAT
13438	27339	A	13582	359	3	KQDSQWVAAPASVAVSTCWRGLPLPWS GGQNRKGKSLPLQVHRGA*GTENKNQGG TPRPGGGPGPSAPRGSSSLGAHRKLPVHH TTLSSRSALPPTPRHPAPSSPPCTEEF HRTRPI
13439	27340	A	13583	174	1	FFFFFFVETESHVAQARVLEYS GAIPAQ

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						CNLDNLSSELPASAS*AS*VAAXTGT*KR
13440	27341	A	13584	192	206	LEFFLEVGSCTVVAQAGFEFFPGSGHLELSA S*VVGSTGVPHHTQLV*SFSSLYNLERN C
13441	27342	A	13585	244	28	KKPENQEINYIFYHLEFNVEHQIRISLGP GAVAYNCNPSTLRD*GGRIT*AQEFKTN LGNMARPRTRGSTRTF
13442	27343	A	13586	312	701	RGPEET*PRTRKSSPRPTRSCESVSKLA RPPRRCSAAPAQVPRLSLRSPKDPDP SSAEKCAPLPLLEPCSETGALPRNSFLC QNASSPLLSLGLPPSPPTVQALQPRALHQ HLGSTNKEDAHVAPAKK
13443	27344	A	13587	410	292	GYMIKQQTVYHECRM*ANSHLHLPPEGL LRAVTLWRRAP
13444	27345	A	13588	428	36	TPPPFFFFWAQKKKKIFPPPGGKIFFFL KGPPPLFFFFFFFFFFFFLKKFGLK GPPFFVQD*QGLENPKEGSSLGWEKLGR ALLPQQRSEFVPGLGPTRLFGLVFWFFG FFFLPFGLCFFFALIFNC
13445	27346	A	13589	3	364	TAPDDQGRPYQAGEPAHVRASTHGLG A*RRVAGHLPPRVGAPHHPGASSREGAP PLHPPPNL*HRRPNGSCRFLPGPAAPPQ GAEGGRGRDRRGTHSVAQTGGPGGFGSG VTPSWRSS
13446	27347	A	13590	778	910	DRIRRSAGAHTCNPSTLGGQGERTA*G QEFKTSLGDMVRFCLY
13447	27348	A	13591	230	3	KLVNIIIVKSLVAMKSTVSEGMVIRSP ASLGMVAHTHSPSTLGGQGRQIA*AQEF ETILGNMAEPCLYKKHSVY
13448	27349	A	13592	223	340	LTPPIPEPWESEVVGSL*LTPGAHTHA YNPRTLGRSGRIT*GHEFQTLSHTMK TRLYHELL
13449	27350	A	13593	35	220	DRASLSPRLCSCGMIVAHCSINLSGSSD PLTPAS*GDGTTDTCHHARLI FTGADFC IDASS
13450	27351	A	13594	87	369	NVQKTECEISGKMQIWQKGSVKTKCSNG LFNFPIFSKKIASCKVKLTRE*KYKSQ ARWCTPVI PATEAEVRGQLEPRSLRP AW ATYQPHFKS
13451	27352	A	13595	261	489	SWVNERNMVG**KHETSQAQWLMPIIPA LCEAEVGGSLARSWETS LCNIVRLHLS KKKRGKGRKRGGNQIAPSRE
13452	27353	A	13596	238	2	NDCLWWLFRIPANVSTFGLLHMSLKVNT PGNNRKFSELGTRCLHTCNPSILGGQG GWIT*GQEFVTSMQGS AVKNQ
13453	27354	A	13597	36	687	RDVHRSTYQAGSKQDWGPGEABRLSSSR RGAYSCPVPITFAEGKTRMGRDKMRLIL GLSWGPSLTLPLITNAPRRPGM*EPAL PGNSTS*SGAVRFPGGGRK*EDSAESWS CFCSHPSPPSGPNPPSPSAVCMPLPGLS GLQR*PKQLSPPPALSLPVSSLLVRLSP WPPTSSHLLPQALPQSLHPQGSRAVND SFSM*GMVLGSRNRRCMEA
13454	27355	A	13598	367	468	KKQRRGREPWLTPTAIPALWAKAGGSP* VQSSRP
13455	27356	A	13599	183	380	LTSMLAVDNSSVEKTCQAMRISRPGAV AHTCNPSILGGQGGLIA*VQEYETNLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MAKTHLYKN
13456	27357	A	13600	161	657	LIQGCWCSLFFSTRVFLAAIGMKSQWCR PVAMDLGVYQLRHFSISFLSLLGTENA SVRLDNSSSGASVVAIDNKIEQAMDVLK SHLMYAV*EEVEVLKEQIKELIEKNSQL EQENNLLKTLASPEQLAQFQAQLQTGSP PATTQPQGTTPPPAQPASQSGGPTA
13457	27358	A	13602	121	423	MIKVNSTGLYLYSQVIYIYIMKYVTAIY LKDFFFDGVLTRHPRWNTVTTQCSEI LGSTDPPASAS*AAGTTNTSHHGQLYSY FKKRPTYAEMEYKIKK
13458	27359	A	13603	1889	1717	VPRIRPLSWTPPSSI*RPKPPSSTFSHP GKPSMGPPGLNRCVPQRRALLPGWYQHCG R
13459	27360	A	13604	81	267	ETCCTKNNTLK*I*SQMLWCAPIVPATW QAEVGGSLDPRSSSL*CAMITSVNNHCT PAWAR
13460	27361	A	13605	267	418	THASGMVTHTCNPGTLRVSAGRIT*GQE FKTSLGNIARPHLYKIIINKYI
13461	27362	A	13606	428	24	CPESNPRKREPTLKSEPIITLPITGLIL DDGNSPTAAAGSVFAETLQPPQCSSLCC* VKSSPWPTASLPQPFSGAPQTLPVRYAL IPGPSLVSTSLGPRAPGLPGSPSPSPSP QVTLDSEYPSPTPCIAPALED
13462	27363	A	13607	267	442	RPPPTLKVPLGVHACNPRTLGGQGG SIS*AQKLENSLSNLRPHLYQKQKQKQ KK
13463	27364	A	13608	3	280	YRLSVICEDPMREREQTCFPPPPSFPN RYCSTRDGGMEGSQGDFRKGFP*APCR SGGGWRGCCSPAGAPGSPLCGSSQGGPV SPWGQKRS
13464	27365	A	13609	291	248	EKRAHGSQPMKGRERNMCKSSSEFRVVA WSLAGVKGDGGR*GSGAGGSPKLG*AV* LDPEGHAGQAVFCGEAGARTQIGGKG*R RDQAPLPLSPNLCSGSCLPTKHS LAMP LRVKSYSQAQLGRTTCTRPSPPTITFDS S
13465	27366	A	13610	267	3	HTDLLYNTPTHPISPRCDPKHTAIPDKQ SLLFFFFEMESCSVARAGVRWHDLRSLR PLPPRF*KFFCCSIPSLYCGRSRGSSQT YTS

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13470	27371	A	13615	197	428	KTMVGLKTSASFHQDFIQIPLNHNLSVP *TMLGSQPRFLFPPGTVSHICNPSTLGG RGGWIT*GQEFETSLATMVKP
13471	27372	A	13616	445	550	TSITRGRARWLTPVILVLWEAEAGGSP* GRSSRLP
13472	27373	A	13617	3	435	TMVLSPADKTNVKAARWVGGAHAGEYGA EALERMFLSFPTTKTYFPHFDLSHGSAQ VKGHGKKEADALTNAAHVDMPNALS VLSDLHAHKLKRVDPVNFKLLSHCLLVTL DRLPAEFTPAVHASLDKFLASVSTVLTS KYR
13473	27374	A	13618	719	918	CEGRREKWKIGRERKGRGRKGEQMGRE GKGREDGGRRKPCTSRPRSSSRDRSNI I ISEHASAVEA
13474	27375	A	13619	847	938	WLMPAVPALLEAEVGISLEAQSCRPPWA TQ
13475	27376	A	13620	349	409	NLWSWPGAVAHVCNPSTLGG
13476	27377	B	13621	25	189	MVLSPADETNNVKAANGKVGAAHAGEYGA EALERMFLCFPTTMTYFPDFDLIHGSAQ*
13477	27378	A	13622	142	356	RIVENEKINAESKSKQKVDLSLPTRAY LDQTVVPIILLQGLAVLAKERPPNPTEFL ASYLLKNKAQFEDRN
13478	27379	A	13623	18	1353	AGAAQCEVVSAGEAGARTMSEADGLRQR RPLRPQVVTTDDGQAPEAKDGSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPID PQPLRQISGIALFCSFKEPPLLLGLVHLP NTKLRQAERLFENQLVGPEISIAHIGDVM FTGTADGRVVKLENGEIETIARFGSGPC KTRDDEPVCGRPLGIRAGPNTLTFVADA YKGLFEVNPWKREVKLLLSSETPIEGKN MSFVNDLTVTDGRKIYFTDSSSKWQRR DYLLLVMEGTDDGRLLDYDTVTREVKVL LDQLRFPNGVQLSPAEDFVLVAETTMAR IRRVYVSGLMKGGADLFVENMPGFPDNI RPSSSGGYVGMSTIRPNPGFSMLDPLS ERPWIKRMIKFLFSQETVMKFVPRYSLV LELSDSGAFRRSLHDPDGLVATYISEVH EHDGHLVYLGSRSPFLCRLSLQAV
13479	27380	A	13624	18	1353	AGAAQCEVVSAGEAGARTMSEADGLRQR RPLRPQVVTTDDGQAPEAKDGSSFSGRV FRVTFMLAVSLTVPLLGAMMLLESPID PQPLRQISGIALFCSFKEPPLLLGLVHLP NTKLRQAERLFENQLVGPEISIAHIGDVM FTGTADGRVVKLENGEIETIARFGSGPC KTRDDEPVCGRPLGIRAGPNTLTFVADA YKGLFEVNPWKREVKLLLSSETPIEGKN MSFVNDLTVTDGRKIYFTDSSSKWQRR DYLLLVMEGTDDGRLLDYDTVTREVKVL LDQLRFPNGVQLSPAEDFVLVAETTMAR IRRVYVSGLMKGGADLFVENMPGFPDNI RPSSSGGYVGMSTIRPNPGFSMLDPLS ERPWIKRMIKFLFSQETVMKFVPRYSLV LELSDSGAFRRSLHDPDGLVATYISEVH EHDGHLVYLGSRSPFLCRLSLQAV
13480	27381	A	13625	1	384	QSFRGTGRKRERERKRMSLSDWHLAAKL ADQPLTPKSIILRLPETELGEYSLGYSI SFLKQLIAGKLQESVPDPFLIDLIIYCGR KLLDDQTLDFYGIQPGSTVHVLKRSWPE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13481	27382	A	13626	980	1089	PDQKPEPVDKEAMRD KRIRIQLTGLYPVPPHPPQSPPIFP RPTSPTRT
13482	27383	A	13627	116	587	VCCELRADSWPVPSQPEQASGPQKQAFI WPEAPRSARLPITYTDYDWSRLQQTQS QMLGSMARKKPRNTSRPLALNPLKSKD VLAVLAERNEAIVPVGAWEVSPSGSSE IPAYTSAYLIEELKEQLRKKQEALKHF QKQVKYRVNQITLRKQ
13483	27384	A	13628	150	484	VAFPPQASRGVRKTEVGEQQGTACGGC GHQCPPTWHIQRACVSTCGAGWHL QGRASCRRPPSQSPQVYQTQVGRQDPHF GVGRDSRGELAWSSFIHYPYLLSVCNPL
13484	27385	A	13629	330	397	ARCEWLTPVIPALWEAEAGGSH
13485	27386	A	13630	10	137	SFTGAVILIIAHGLTSSLLFCLANSNYE RTHNLFFLNDFFFS
13486	27387	A	13631	380	98	FQWLVSFTATLWFEERHRKNKIEREERR AKGERGDRKEERREEGGERGRRGGERS DKREPKKKSKEESNHPKVVFSCFICSFC FLTPFFPVFF
13487	27388	A	13632	56	827	PLFEAFTACGFVHDCGLLIHPEETCGLO PISSDYIEAILQSELKRCPSGDMKGQWI VPCLSCSDNRTCDWREITWQPHNCQYGV LTKPQLQQCLGGRKILFIGDSTNRGIMY YLIERLNETLQEWQKVHGTGFYHNVNGG KTLISYSYYPQFWISPSLRPTFENALEH LLQRSRPLENTGQTVLVVGGVQWLNSNH LQIIHKVLKSPFTTLNQPVTKSCLQAIY FPRLSPTLHSNCLDLVSFTKSFNIYFV VQFLN
13488	27389	A	13634	3	2718	SGPCRTTVAPLLRAAPVEHCVAALRPTD STMLKKFDKKDEESGGGSPFQHLEKSA VLQEARVFNETPINPRKCAHILTKILYL INQGEHLGTTEATEAFFAMTKLFQSNPD TLRRMCYLTIKEMSCIAEDVIVTSSLT KDMTGKEDNYRGPAVRALCQITDSTMLQ AIERYMKQAIVDKVPVSVSSALVSSLHL LKCSFDVVKRWVNEAQEAASSDNIMVQY HALGLLYHVRKNDRLAVNKMISKVTRHG LKSPFAYCMMIRVASKQLEEDGSRDSP LFDFIESCLRNKHEMVVYBAASAVNLIP GCSAKELAPAVSVLQLFCSSPKAALRYA AVRTLNVKVMKHPSAVTACNLDLENLVT DSNRSIATLAITTLTKTGESESIDRLMK QISSFMSEISDEFKVVVVQAISALCQKY PRKHAVLMNLFFTMLREEGGFEYKRAIV DCIISIIIEENSESKETGLSHLCEFIEDC EFTVLATRILHLLGQEGPKTTNPSKYIR FIYNRVVLEHEEVVRAGVSALAKFGAQN EEMLP SILVLLKRCVMDDEVRDRATF YLVNLEQKQKALNAGYILNGLTVSIPGL ERALQQYTLEPSEKPFDLKSVPLATAPM AEQRTSTPITAVKQPEKVAATRQEIFQ EQLAAVPEFRGLGPLFKSSPEPVALTES ETEYVIRCTKHTFTNHMVQFDCNTNLN DQTLNVTVMQEPTEAYEVL CYVPARSL PYNQPGTCYTLVALPKEDPTAVACTFSC MMKFTVKDCDPTTGETDDEGYEDEYVLE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DLEVTVADHIQKVMKLNFEAAWDEVGDE FEKEETFTLSTIKTLEAVGNIVKFLGM HPCERSDKVPDNKNTHLLLAGVFRGGH DILVRSRLLLDVTVMQVTARSLLELPV DIIILASVG
13489	27390	A	13635	118	629	LWALQLHPEPELPSRRGTGAAGVWTGVA MIRFILIQN RAGKTR LAKWYMQFDDDEK QKLIIEVHAVVTVRDAKHTNFVEFRNFK IIYRRYAGLYFCICVDVNDNNLAYLEAI HNFVEVLNEYFHNVCLELDLVFNFKVYVT VVDENFLAGEIRETSQTKVLKQLLMLQS LE
13490	27391	A	13636	57	221	LHHCTPPWAEVEETLKR LQSQKG VQGII VVNTEGGWEPLGHCGDRSRPPAQGCP
13491	27392	A	13639	344	544	LSGGHAGALSSSLWVHLYCLLSQQLLGN VLVTVLAIHFGKEFTPEVQASWQKMTG VCSALCFRYH
13492	27393	A	13640	319	623	DMEEASEGGGNDVRNLQSEVEGVKNIM TONVERILARGENLEHLRNKTEDLEATS EHFKTTSQKVARKFWWKNVKMIVLICVI VFIIILFIVLFATGAFS
13493	27394	A	13641	2099	769	TRLAGRVSVASRPCRGPAVGGLLVERSK ARRPLLESERVAMAAPPELLQQEEDRSK LRSVSVDLNVDP SLQIDIPDALSERDKV KFTVHTKTTLPTFQSPEFSVTRQHEDFV WLHDTLIETTDYAGLIIPPATKPD F DG PREKMQLGEGEGSMTKEEFAMKQELE AEYLAVFKKTVSSHEVFLQRLSSHPVLS KDRNFHVFL EYDQDLSVRRKNTKEMFGG FFKSVVKSAD E VLF TGVKEVD DFFEQEK NFLINYYNRIKDS CVKADKMTRSHKNVA DDYIHTAACLHSLALEPTVIKKYLLKV AELFEKLRKVEGRVSSDEDLKLT ELLRY YMLNIEAAKDLLYRRTKALIDYENS NKA LDKARLKS KDVKLAEAHQQECCQKFEQL SESAKEELINFKRKRVA AFRKNLIEMSE LEIKHARNNVSL LQSCIDLFKNN
13494	27395	A	13642	210	772	SVKMVRYSLDPENPTKSCSRGSNLRVH FKNTRETAQA IKG MHIRKATKYLKDVT L QKQCVPFRRYNGGVGRCAQAKQGW TQG RWPKKS AEFLHMLKNAESNAELKGLDV DSLVI EHIQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVPKPEEEVA QKKKISQKKLKKQKLMARE
13495	27396	A	13643	168	2172	SPLCEVSVPSFCFRVFCCKHKKHKS D KH LYEEYVEKPLKLV LKVG GNEVTELSTGS SGHDS S L F E D K N D H D K H D R K R K R K K G EKQIPGEEKGRKRRRVKEDKKKRD RDRV ENAEKDLQCHAPVRLDLPPEKPLTSSL AKQEEVEQTPLQEALNQLMRQLQRKDPS AFFSFPVTDFIAPGYSMI IKHPMDFSTM KEKIKNDYQSTIELKDNFKLMCTNAMI YNKPETIYYKA AKKLLHSGMKILSQERI QSLKQS IDFMADLQKTRKQKGD T DTSQS GEDGCGWQREREDSGDAEAHAFKSPSKE NKKKDKDML EDKFKSNNLEREQEQLDRI VKESGGKLT RRLVNSQCEFERRKPDGTT TLGLLHPVDP I VGE PGYCPVRLGMTTGR

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						LQSGVNTLQGFKEDKRNKVTPLVLYLNVG PYSSYAPHYDSTFANISKDDSDLIYSTY GEDSDLPSDFSIEFLATCQDYPYVMAD SLLDVLTGKGHSRTLQEMEMSLPEDEGH TRTLDTAKEMEQTETEVEPPGRLDSSSTQD RLIALKAVTNFGVPVEVFDSEAEIFQK KLDETTRLRELQEAQNERLSTRPPPNM ICLLGPSYREMHLEQVTNNLKELAQQV TPGDIVSTYGVKAMGISIPSPVMENN VDLTEDTEEPKKTIDVAECGPGGS
13496	27397	A	13644	1032	207	PADVTPKPATEAVQSEHSASPMSINEV ILSASGACKLIDSLHSYCFSSRQNKSQV CCLREQVEKNGELKSLRQRVSRSDSQV RKLQEKLELRRVSVFPYSSLLSPSREP PKMNPVVEPLSWMGLTWLSDPPGAGTYP TLQPFQYLEEVHISHVGQFMLNFSFNSF HPDTRKPMHRECGFIRLKPDTNKVAFVS AQNTGVVEVEGEVNGQELCIASHSIAR ISFAKEPHVEQITRKFRNLNSEGKLEQTV SMATTTQPMTQHLHVTYKKVTP
13497	27398	A	13646	148	380	RGSWREVPEASLPSRGAKGKWRGLCCC CCCCCCCCCYHCHQEQGDLKHQADL WRSGRTQNQAGIWQEHQTLEG
13498	27399	A	13647	2099	769	TRLAGRVSVASRPCRGPVAGLLVERS ARRPLLESRVAMAAPPELLQQQEEDRSK LRSVSVDLNVDPSLQIDIPDALSERDKV KFTVHTKTTLPFTFQSPEFSVTRQHEDFV WLHDTLIETTDYAGLIIPPAPT KPDPDG PREKMQKLGEGEGSMTKEEFAKMQBLE AEYLAVFKKTVSSHEVFLQRLSSHPVLS KDRNFHVLFLEYDQDLSVRRKNTKEMFGG FFKS VVKSADDEVLTGVEKVDFFFEQEK NFLINYYNRKIDSCVKADKMTRSHKNVA DDYIHTAACLSLALAEPTVIKKYLLKV AELFEKLRKVEGRVSSDEDLKLTLLRY YMLNIEAAKDLLYRRTKALIDYENSNKA LDKARLKSVDVKLAEAHQEQECQKFBQL SESAKEELINFKRKRVAAPFRKNLIEMSE LEIKHARNNVSLQSCIDLFKNN
13499	27400	A	13648	1	1206	MSTSQSPCESICDYVTSHEKSNFTDMIK LNILRCEVILDYPAPGGGSLGAKHCCSC YTVSSGVTEGERNAGEKGVKLNADGARI RGTPGRGRRAEAEASSPAPA AAVAAACVV AAAAASRQLASGNRTRVSSGVPAFLG TMNPNCARCGKIVYPTKVNCLDKFWHK ACFHCETCKMTLNMKNYKGYEKKPYCNA HYPKQSFTMVADTPENLRKQQSELQSQ VRYKEEFKNGKGFVSVADTPQLRIK KTQDQISNIKYHEEFKSRMGPSGGEGM EPERRDSQDGSSYRRPLEQQQPHHIPTS APVYQQPQQQPVASQSYGYKEPAAPVSI QRSAPGGGKRYRAVDYSAADEDEVSF QDGDITIVNVQQIDDGWMYGTVERTGDTG MLPANYVEAI
13500	27401	A	13649	3	394	GDGGGHLGSGRNGGSGMNAPPAFESFLL FEGEKITINKDTKVPNACLFMTNKEDHT LGNIIKSQLLKDPQVLFAGYKVPHPLEH KIIIRVQTTDPDYPQEAFTNAITDLISE

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13501	27402	A	13650	1	471	LSLLEERFRVRAGPGGAD SRPTGLREAGSGPREAPRRSGCKSPGL GTVGMLRPKALTQVLSQANTGGVQSTLL LNNEGSLLAYSGYGD TDARVTAASNI WAAAYDRNGNQAFNEDNLKFLMDCMEGR VAITRVANLLLCMYAKETVGFGLKAKA QALVQYLEEPLTQVAAS
13502	27403	A	13651	1334	82	CYTGGTQSLWPGSSCASSVARPSSLFRS AWSCEWSVRCARACTMSVPAFIDISEED QAAELRAYLKSKEAIESENSEGGHLVD LAQII EACDVLKEDDKOVSMNSVVS LLLILEPDKQEBALIESLCEKLVKFREGE RPSRLQLLSNLFHGMKDNTPVRYTVYC SLIKVAASCGAIQYIPELDOVRKWISD WNLTTEKKHTLLRLLYEALVDCKSDAA SKVMVELLGSYTEDNASQARVDAHRCIV RALKDPNAFLFDHLLTLKPVKFLEGELI HDLITIFVSAKLASYVKFYQNNKDFIDS LGLLHEQNMAMRLLTFMGMAVENKEIS FDTMQQELQIGADDVEAFVIDAVRTKMV YCKIDQTRKVVVSHSTHRTFGKQWQQ LYDTLNAWKQNLNKKVNSLLSLSDT
13503	27404	A	13652	1	377	TTASGRSGVKGSTMSAEVPEAASAEQK EMEDKVTSPKAEAEAKLKARYPHLGQKP GGSDFLRKRLQKGQKYFDSGDYNMAKAK MKNKQLPTAAPDKTEVTGDHIPTPDLP QRKPSLVASKLAG
13504	27405	A	13653	424	596	SLKNIYGLSCRKKKKGAVKKIILVQAWW LMPVITVLWEAEVGGLEARGLRPTRAT W
13505	27406	A	13654	190	448	LRSYPAPHLGSPELRIRKGRGHSHCLAG AAGPQRTALCGLSAPLCPPSPTPGAGA PRYCSGSDAPPCLLRGAGPPIPGMGDPE TS
13506	27407	A	13657	1612	563	SMPGWRLLTQVGAQVLGRLGDGLGAALG PGNRTHIWL FVRGLHGKSGTWDEHLSE ENVPPFIKQLVSDDEKAQLASKLCPLKDE PWP IHPWEPGSFRVGLTALKLGMPLWT KDGQKHVVTLQVQDCHVLKYTSKENCN GKMATLSVGKTVSRFRKATSILEFYRE LGLPPKQTVKIFNITDNAIKPGTPLYA AHFRPGQYVDVTAKTIGKGFQGVMKRWG FKGQPATHGQTKTHRRPGAVATGDIGRV WPGTKMPGKMGNIYRTEYGLKVWRINTK HNIIYVNGSVPGHKNCVLVKVDSKLPAY KDLGKNLPFPTYFPDGDEELPEDLYDE NVCQPGAPSITFA
13507	27408	A	13658	128	2626	NSHRWVYVRARRRRRGKQREQPEDRGV PMKRAAMALHSPQYIFGDFSPDEFNQFF VTPRSSVELPPYSGTVLCGTQAVDKLPD GOEYQRIEFGVDEVIEPSDTLPRTSYS ISSTLNPQAPFIFLGCTASKITPDGKITK EASYGSIDCQYPGSALALDGSSNVEAEV LENDGVSGGLGQRERKKKKRPPGYYSY LKDGGDDSI STEALVNGHANSAPNSVS AEDAEFMGDMPPSVTPRTCNSPQNSTD VSDIVPDSFPFGALGSDTRTAGQPEGGP GADFGQSCFP AEAGRDTLSRTAGAQPCV

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						GTDTTENLGVANGQIILESSGEGTATNGV ELHTTESIDLDPKPEASPPADGTGSA SGTLPVSPQKSWASLFHDSKPSSSPVA YVETKYSPPAISPLVSEKQVEVKEGLVP VSEDPVAIKIAELLENVTLIHKPVSLQP RGLINKGNWCYINATLQALVACPPMYHL MKFIPLYSKVQRPCTSTPMIDSFVRLMN EFTNMPVPPKPRQALGDKIVRDIRPGAA FEPTYIYRLLTVNKSSLSEKGRQEDAE YLGFILNGLHEEMLNLKLLSPSNEKL ISNGPKNHSVNEEEQEEQGESEDEWEQ VGPRNKTSVTRQADFVQTPITGIFGGHI RSVVYQQSSKESATLQPFFTLQLDIQSD KIRTVQDALES LVARESVQGYTTKTKQE VEISRRVTLEKLPVVLVHLKRFVYEKT GGCQKLIKNI EYPVDEISKELLSPGVK NKNFKCHR TYRLFVAVYHHGNSATGGHY TTDVFQIGLNGWLRIDDTQTVKVINQYQV VKPTAERTAYLLYYRRVDLL
13508	27409	A	13659	42	382	TLWLKTIQIYLTISLGLGSDYGLAGFSA LGCHQAAVKMLTAFILIQGLDLGRSHFQ AHSGCWQDSFPCDSRIHGGLLLHVQQES PWFQSAERVSCITKCNHRSDTHLLCSIL L
13509	27410	A	13660	178	349	DMGPCYVAQTVLKLGLSSDPPTSASQEA GTTCHHAHLLSHPFLLMIYRNFSTIQCLE T
13510	27411	A	13661	268	2	RQQKVILSSSGSLMSEMGRITVLPKSPG MNPSSPLLASGGCWKSLACGHII PFSSF ILMWPSPLCVSVSSSLPMRKPLLHLRS TLFQ
13511	27412	A	13662	112	483	AGVGALRMVQRLTYRRRLSYNTASNKTR LSRTPGNRIVYLYTKKVGKAPKSACGVC PGRLRGVRAVRPKVLMRLSKTKKHVSRA YGGSMCAKCVDRDIKRAFLIEEQKIVVK VLKAAQSQKAK
13512	27413	A	13663	2	873	SVEEFDRGCTGRGCGADARAGAAMVKIS FQPAVAGIKGDKADKASASAPAPASATE ILLTPAREEQPPQHRSKRGSSVGGVCYL SMGMVLLMGLVFASVIYRYFFLAQLA RDNFFRCGVLYEDSLSSQVRTQMELEED VKIYLDENYERINVPVPQFGGDPADII HDFQRGLTAYHDISLDKCYVIELNTTIV LPPRNFWE LLMNVKRGTYLPQTYIIQEE MVTTEHVSDKEALGSFIYHLCNGKDTYR LRRRATRRRINKRGAKNCNAIRHFENTF VVETLICGVV
13513	27414	A	13664	118	3	AWSLIPVIPVVREAKAGGLLEPRSLRPT WATWQDPVST
13514	27415	A	13665	1	2876	IRQRINFSRKNKWD SRKLDQAGVSELAT NQKLILVCGRYEGIDERVITQTEIDEEWS IGDYVLSGGELPAMTLIDSVSRFIPGV GHEASATEDSFAEGLDCPHYTRPEVLE GMEVPPVLLSGNHAEIRRWRLKQSLGRT WLRPELLENLALTEEQARLLAEFKTEH AQQQKHHDGMAADEAGRTFLRADFNMI EGDRI MVCLSGGKDSYTMLEILRNLQQS APINFSLVAVNLDQKQPGFPEHVLPEYL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EKLGVEYKIVEENTYGVKEKIPGKTT CSLCSRLRRGILYRTATELGATKIALGH HRDDILQTLFLNMFYGGKMKMPKLMMS DDGKHIVIRPLAYCREKDIQRFADAKAF PIIPCNLGCSQPNLQRQVIADMLRDWDK RYPGRIETMFSAMQNVVPSHLCDTNLFD FKGITHGSEVVNGDGLAFDREEIPLQPA CWQPEEDENQLDELRLNVVEPDGPRHRH APDARRFCQYLRHQARYLLSVVPNLDVA VTEPLANGDGLNVLKREVVGFRAITVE KTGENQYRVWPNEMPADLHKIRPHHPLN RNLDHFFPLDLTNSTFSGGYVHVLKGV SDDLKLSFKQMGYVRRDSHRLMVTALP PACQLVQVALGCFALRLECEILGEVLAQ LGTSVLPAEELLQARRASGDVASCQRLA QDEEPPLPPRGSPAAAYRAPLDLYRDLQ EDEGEDASLYGEPSPGPDSPPAELAYR PPLWEQSAKLWGTGGRAWEPPEELPQA SSPPYGALEEGLEPEPSAFSFLSLRREL SRPGDLATPESSAAASPRRIRAEVGPAS AYRSVSEPPGYQGTQLPVPWRPAHPLLR HLSPAACCPLCSPARLPSPRLAACAAWR RPAALVATACTDGHSAQQPRGPALGQL GPRSRLGRQLPWCFSLLGRGLGLWLPFC PWGSPGHSRGLSPGQPLLEVGLSVYGR LQQQQA
13515	27416	A	13667	76	289	SGTFASPCEMDPNCSCSPVGSACAGS CKCKECKCTSCCKSCCSCPVGCAKCAQ GCICKGTSKDCSCCA
13516	27417	A	13669	2	667	GRVDAEQSRLGATERAAAAAMNPEYDYL FKLLLLIGDSGVGKSCLLLRFADDTYES YISTIGVDFKIRTIELDGTIKLQIWDT AGQERFRTITSSYYRGAHGIIIVVDVTD QESYANVKQWLQETDRYASENVNKLVLG NKSDLTTKKVVDNNTAKEFADSLGIPFL ETSAKNATNVEQAFMTMAAEIKKRMGPG AASGGERPNLKIDSTPVKPAAGGCC
13517	27418	A	13670	176	398	RILKTQLQENNQPTTTTKNRQKTRTDTL PKGIYRRHISLWKLGTWLTVPVIALCEA NAGGRLESRSRPVWATY
13518	27419	A	13671	149	247	RKGLALSPRLDCSGAITVNCSLNLQGLS NIPI
13519	27420	A	13672	257	359	VASLHGWAQWLTPVIPTLWKTKEVGEFFE PRCSR
13520	27421	A	13673	142	1	HLKGSGLAKHQWLMPVIPALWEAEVGG LEPRSSRPVWATLQDPIS
13521	27422	A	13674	619	168	MFIESCTPKIYTSFVLRQSHSFAQAGV QWLDLGSLOPLSLGSSNSPASASCIQVL FVIYTSVKLGVGGRLLGNKKVMSSNKKFV CECRGWIILPFSVPSLRFQDGGWDHGV SAEKALQAGRTAGHRVGVPLGAPCGGA PCTTPPAWRS
13522	27423	A	13675	3	370	ARALLHPRLHQWQCLCHLQGTGGCPQQS PSSEGRADLLSPALEEGYPPPASGCFIP HFLCGCSIFNCLPPIMRHAHKS PDALLE TLGPCRAWRLMPVIPTLWEAKVDRILLES RSSRPSWPTW
13523	27424	A	13676	3	281	IGLRPELSVSLGRQRLTAIRLQPLLPAR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPCGFLRARVAIALMADETDLPPLPRLE YSGMITAYCSLDFLGSSDPPTLGSGVAG TTENCCED
13524	27425	A	13677	272	389	YCRQIEKSKKKRCWLGTVAHACNPSTWG GRGGRITRSRD
13525	27426	A	13678	261	363	NSSWGHRWLTSVIPALWEAEVGGSPPEV RSLRPV
13526	27427	A	13679	149	44	SCVMSVSVLKKMYWLGAVAHACNPSTLG GQGGRTA
13527	27428	C	13680	118	267	MSHCTWLMCVVCVCVCVCVYAYMYTYSF LRWDLPLMLSRLECSGSQAQ**
13528	27429	A	13682	16	346	NHHLTQPHPHLDINDFFFFFFFFFFFFFFF FFFFFFFFFFFFLKKSPRAGKKKKKKKK KKKPPRFFFLGGAPPLFFFLINFFFFFF LCKIISLVYNRRGGPCLSKRFFLKERKS PL
13529	27430	A	13683	244	140	GRVDVFHHVAQAGLKLSSGDLPAWPPK ELRLQV
13530	27431	A	13684	191	777	NSDEHVYRCLYGHKLSFLSKYLKSGLA GVLLPLDAAVDMKEIEEQFANLHIVKCS LGTKEPTYLLGIDTSKTVOAGKENLVA LCSNGSIRIYDKERLNLREFSGYPGLL NGVRFANSCDSVYSACTDGTVKCDARV AREKPVQLFKGYPSNIFISFDINCNDHI ICAGTEKVDLALFGGFGDARMEFLQN
13531	27432	A	13685	150	253	VGWGLWLVVIPAFWEAKMGESLDPRNL LPCWAT
13532	27433	A	13686	500	321	IEMGSHYVAQAGLELLSSSNPPTSVSQS AGIVGMSHHALAAISKSSDASITSHHPM TTP
13533	27434	A	13687	6	424	MSLLQCGGIRCFKMPEPAKSAPAPKKGS KKAVTKAQKKGKRRKRKESYSVIVY KVLKQVHPDTGISSKAMGIMNSFVNDIF ERIALGEASRLAHYNKRSTITSREIQTAV RLLPLGELAKHAVSEGTKAVTKYTSSK
13534	27435	A	13688	178	293	TGYSSQAQWLMTVLATWEAEAGGSIQP RSLRPAAWTQ
13535	27436	A	13689	663	144	KELSAVSAGIPHSCGSGCGGGGVAACV PAAPAAAGLCSGRAQKVPVPPSLAGWPP GVNAPPPVCSVRLHVCQSDRLWVRLA ARRGILALLRSALKAAATLAGCQSVRWSV RPSESLRPTSNAASLFRSSVPTVLSHSV PLAASLGKRRACGGREHASVAVYLSVCL SLPT
13536	27437	A	13690	125	3	FAHQGHAPGQAWLRLPVPVLRREELGG RPEPRSSRTARA
13537	27438	A	13691	136	24	GGPPPPPPPPPPPPPPPPPPPPPPPPPP FFPGKLQQDFQYYVK
13538	27439	A	13692	144	1	MLKIVQSGECLTLKFNFCLLSLCTLFP TLIALTTLLLPISPFILIL
13539	27440	A	13693	1476	380	NSWSTLASELTWAATSADPERKSQAAS AAMWATLPLLCAGAWLLGVPVCGAELC VNSLEKHFHFKSWMSKHKRTYSTEEYHHR LQTFASNWRKINAHNNGNHTFKMALNQF SDMSFAEIKHKYLWSEPQNC SATKSNYL RGTGPYPSPVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALSAIAIATGKMLSLAE QQLVDCAQDFNNHGCQGLPSQAFEYIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						YNKGIMGEDTYPYQGKDYCKFQPGKAI GFVKDVANITITYDEEAMVEAVALYNPVS FAFEVTQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGEKNGIPYWIWKNSWGPQ WGMNGYFLIERGKNMCGLAACASYPIPLV
13540	27441	A	13694	87	2	PGWAWWFTPVILALWETEAGGSPEFKSL
13541	27442	A	13696	130	2	CNIIIIIIQVCWAWWLMFPVIALWHAEP GGSPEVESSRPALV
13542	27443	A	13697	282	107	GLTKCPGTVCRLKVVVISYQLSIICLSM MEHSGTILAHCSLKLGLSSDPPTSRSRV AS
13543	27444	A	13698	198	3	CSITVNKVKVMTLFRSSMSLEIVCDIDL AVLRDLGLSLQDPPFRFTPLSCLSLPSS WDYRRPLV
13544	27445	A	13699	2	120	ARGDGVSLWLPRLKCNAGTSAHCNLRPT GSSDKNFKTRF
13545	27446	A	13700	60	341	PDMGLEDERKMLTESGDPEEEEEQEEL VDPLTTVREQCEQLQKCVKARERLELCD ERVSSRSHTDDDCPEELDFLHAKDHCV ALKLFNNLQ
13546	27447	A	13701	6	540	KNSRTLGCQGGIRGSLCRPKPGVGGTQ TRAVRPVAVCSADSARPHLPLRRADMKDS LVLLGRVPAHPDSRCWFLAWNPAAGTLLA SCGGDRRIRIWGTGDSWICKSVLSEGH QRTVRKVAWSPCGNYLASASFDATTCIW KKLTLRIYNILRKLEACIKPLCCALKYK CLEEKQLHS
13547	27448	A	13702	239	346	AKRGWLMFPVIALWEAKVGKSLERPRIS PLWATWQN
13548	27449	A	13703	210	300	LMPVISALWEAKARGLLEPRTLPAWAT W
13549	27450	A	13704	141	440	PSAFEHFEEKINLYFLKFCISQGFPERQN NRDREIHRERYERDRERHRYERGLRE LAHVIVEAEKPHHRPFITWETLGCWWSG SVQVQKWPWEPGKLMV
13550	27451	A	13705	204	438	LLNVLLTQLFFLFLSLRQSCSVAQARGQ WYNHGSLQPSHSGASNPPTSASQSVGTT GMSHDHGLFLHFSTLDIFSSL
13551	27452	A	13706	1707	1821	AKAGGSQHLEILANAVKPCLYWECKMAG PWWCAPVGG
13552	27453	A	13707	167	334	IRRANFKILTEIGWTQWLTPVIALWEA EGGGLLLEPGSPSLVFLFFILTTILMRKK
13553	27454	A	13708	224	344	KDTAMEEEIKDTEKTGKRWLGAVAHACN PSTLGDQGRQIA
13554	27455	A	13709	1476	380	NSWSTLASELTWLAATSADPERKSQAAS AAMWATLPLLCAGAWLLGVPVCGAAELC VNSLEKPHFKSWMSKHKRTYSTEEYHHR LQTFASNWRKINAHNNGNHTFKMALNQF SDMSFAEIKHKYLWSEPQNCSTKSNYL RGTGPYPSPVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLSLAE QQLVDCAQDFNNHGCQGLPSQAFEYIL YNKGIMGEDTYPYQGKDYCKFQPGKAI GFVKDVANITITYDEEAMVEAVALYNPVS FAFEVTQDFMMYRTGIYSSTSCHKTPDK VNHAVLAVGYGEKNGIPYWIWKNSWGPQ WGMNGYFLIERGKNMCGLAACASYPIPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						V
13555	27456	A	13710	763	257	YEKILKLTADAKFESGDVKATVAVLSPILSSAAKHSVDGESLSSELQQLGLPKEHAASLCRCYEEKQSPLQKHLRVCSLRMNRLAGVGWRVDYTLSSSLLQIRGKSPWCHCGWKVATCPQGPQAPACLPFPSSKTKFPRSSLARTESRPKTLMKLPWAEKGVPRPV
13556	27457	A	13711	133	401	VLSKSGNPYWGLSTNHEIKGQEGCAWQLTPVIPALWEAEAGGSLEPRSLRPANATSWLPREIKLDDLKNGCGPSKITQGGPMVAGSLKL
13557	27458	A	13712	212	74	RRINLAPPRVFLKGPPFFFFFFFFFFFFFFFAWGNPLFLFNSTFGRT
13558	27459	A	13713	324	141	DRVLPRLCSCGVITARYRLNLLGSRDPPTSASLIAGSTGTCHHAWLSFSYLFYVFFIIL
13559	27460	A	13714	299	431	IRLIWLSAVDHACNSSTLGGHGVQMTKGQDFETNLANTANPHPY
13560	27461	A	13715	133	1	ILVWAWWDMPAIPVLWEAETEGLEPRSLRPAWATWKNTISTKN
13561	27462	A	13716	18	165	IPLHTHTHTHTHTHTHTGYLLALSGTEFLSVLYMASERECRTYNMLNK
13562	27463	A	13717	119	1	KPNVSAQWLAPVIPALWEARVGVLFKPRSLRPTWATQQ
13563	27464	A	13718	271	64	VLRISITLNEILAKTRNPPLQILMKPRKRWGTVAHLRAPVGDQPDQHSETPSLLKTKISWVWWRTPVI
13564	27465	A	13719	21	209	KDGPKGTTGGSETNESVEMTECCSVTQAGVQWHDLSLQPPPPGFKRFSCLGLPSSWDYSRND
13565	27466	A	13720	391	151	RGFFLKGEKKKNFFPIILGKKILGSPGKKGKKKKKRGKIFFFLKNPLGFFPKKKVLGEKKNPYSGVWGGKKKRGPPPH
13566	27467	A	13721	109	2	RRLGVVAHACNPSTLGGEVGGSGQPGNCQGVTKVS
13567	27468	A	13722	69	369	RDILQADGAHSLFPTTPSLNAYIIFSSPIGPHTHRPHYATPTYLPFYTNLLIKKKKKKKKKKKKKKKKKKKKKGGGPKKTPGGAPIFGGGGK
13568	27469	A	13723	58	1208	FWNENSPASELAPNGGGSVTSVPRLEDYLTRPQLYKLTGVEGPSRANSRDSFHDRKTYKTPSANMMVLKVEELVTGKKNGNGEAGEFLPEDFRDGEYEAATLEKQEDLKTLLAHPVTLGEQOWKSEKQREAELEKKKLEQRSKLENLEDEIIIIQLKKRKKYRKTVPVVEKEPEPIITEPVDVPTFLKAALENKLPVVEKFLSDKNNPDVCDEYKRTALHRACLEGHLAIVEKLMEAGAIIEFRDMLESTAIHWASRGGLDVLKLLNKGAKISARDKLLSTALHVAVRTGHYCAEHLIACEADLNAKDREGDTPHDAVRLNRYKMIRLLIMYGADLNIKNACAGKTPMDLVLHWQNGTKAIFDSLRENSYKTSRIATF
13569	27470	A	13724	400	135	KWNGKELNGVDGIGWDWNEMYWKGLEFHETEWNELERNGLEWNGMSWDGIKCNIGIKWNGIECSGMLWNGMECIGMECPLMEWIRVEWN
13570	27471	A	13726	186	344	SASLGLWRCRDCRRSLVHSLNVAQAGV

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						QWRDLSSLQPPPPSRLPWPPKVLR
13571	27472	A	13727	380	168	APPQKKVFGSKFPQGGFFAPPNRKKLFF SPPRKIVPPPKFFLWAPLFFFFFFF FFFFFFFWYSRTDYK
13572	27473	A	13728	324	219	RIMFFIFFYFFFFFFFVFFLFFFFFKR PPFFFY
13573	27474	A	13729	2	270	RLQEASLSPVPEILGGALPSAKRTSYLL LSTLCLLLSETASRGNSLTGLGHRSDHY NSVRSGGQSLYSACPIVTIHGTCYGGK AKCK
13574	27475	A	13730	134	3	AVHRCKKWGRGWRLTPVIPTLWEAEV GGPLEPRSLRPALAT
13575	27476	A	13731	429	641	RKKAVCFMNDLICFLDNIFKNNVLSQAW WCVHLVPTIWEAEAGGSLEPRSLKLQCP VVAPVNNCTPAWAT
13576	27477	A	13732	188	32	IFFFFLFFYLFLLLLFFPRSRHCTLQP GQQSETRSQNKQKTKNKQTKNLP
13577	27478	A	13733	341	3	GTVTPEEPKMGDQTPRGLRPERTLGR LSTSESVDPTPRVGGSSGGRTAPWGP PRERGRVAGSSLHRACNFSTNTIISVG LWLTPIVPTLGEAEAGGSPEVRSSTHAS
13578	27479	A	13734	208	2	KLYKNFFFRFTKNPPLLKKGFYLYNFF FKKKKKIVKKKKKKKKKKQKKKKKK GRPLAIKNYPRV
13579	27480	A	13735	16	212	EGVSLLLPRLECRGTISAHCNLRHRGRR CTPASASQILRLKQENHLNLGGGYRD PIKLQRTAS
13580	27481	A	13736	22	214	PDRPALPTRPGGWITWGREVRDQPGQCG ETPSLLKIEKLAGCDGTCLEQNCLQNNN SNNKVGIR
13581	27482	A	13737	386	51	WNSITQQALFEHLCSGHTSLPAVPCP HQACFPTLPLICRGIIAHCNLGLLGSS DSPISASPIDGNTGLHPHARLFSPLWY RWGLTMMPKRSLSPGLKPSSRLADAWV
13582	27483	A	13738	204	431	SQHFGISRADHLSSNVGDQPEQHGNKS LYKYYKINQGWAWWLTVPVPLWEGQVG GSPEGKELKTPLRNLGKPHL
13583	27484	A	13739	69	159	IKKEALSWAWWLTVPVLPALWKANAGGSP E
13584	27485	A	13740	32	285	FFLSFFLFFFFFFGGGKKTKKFFSQD FLGPPKILGGGGFFSFFGCPFLKKGK KSPQNLFFLKKNPPFFFPKPLWGF
13585	27486	A	13741	372	213	YRSCVLLQONPPLFYQSWWNFSLCVCVC VCVCVCVCETGSLKKFLLTQKKKR
13586	27487	A	13742	29	237	TKRKGYKTNKGYWAWWLTVPVLPALFI AEGNLIQMQKQAQPEAGCGVCVCVCA CMCVCVCVKVFF
13587	27488	A	13743	322	183	HTHTHTHTHTHTHTNPIHVFLLLLKY PKIQSHQFHISAFQDPLL
13588	27489	A	13744	305	373	VGWGWLTVPVLPALWEAKVGGG
13589	27490	A	13745	172	1	KNKIEQMKWEMRQEAVAHSCNPSTLGG QGEFETSLVNMMPCLYKKMQKISQVCS C
13590	27491	A	13746	285	1045	FQHPFGLSQSEMAAVKASTSKATRPWYS HPVYARYWQHYHQAMAWQSHNAYRKA VESCFLNPWYLPALLPQSSYDNEAAYP QSFYDHHVAWQDYPCSSSHFRRSQHP YSSRIQASTKEDQALSKEEMETESDAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VECDLSNMETTEELRQYFAETERHREER RRQQQLDAERLDSYVNADHDLYCNTRRS VEAPTERPGERRQAEMKRLYGDSAAKIQ AMEAAVQLSFDKHKCDRKQPKYWPVPLK F
13591	27492	A	13747	2	305	GRVGSFSVRDVELSDPARERGEMPVAVG PYGQSQPSCFDRVKMGFVMGCAVGMAAG ALFGTFSCLRIGMRGRELMMGGIGKTMQ SGGTFGTFMAIGMGIRC
13592	27493	A	13748	2	305	GRVGSFSVRDVELSDPARERGEMPVAVG PYGQSQPSCFDRVKMGFVMGCAVGMAAG ALFGTFSCLRIGMRGRELMMGGIGKTMQ SGGTFGTFMAIGMGIRC
13593	27494	A	13750	238	423	AVSWDQLTWGTGVQEKKIQAQAWGLMPV IPTLWEVEVGGSPVKSRRPACPHGKTP FLLKMQ
13594	27495	A	13751	455	248	ISVGPGLFQNLNFCLEPYGTFLLSEKFF IMETGSRFVIQAGVQWGSYSSPQPQFFG FESSLKPPHSGVK
13595	27496	A	13752	2	98	IPTPTIHTHTSHHTHTHTHTSFLYMP PDLK
13596	27497	A	13753	196	2	IWAPPKIFLKKPPLFFFFFFFFFFFFFFF FFFFFFFFIISFIPWPLTRKQKLSRWVF FKDSACSA
13597	27498	A	13754	917	379	KYKKCSLQKNLLLVGCKKYSYLCYRREKL HLVTHGERKKPAAVNSFFLFFSFFFLN LVRNTEITKKRVNLHETKADAESCNDQC TTSSETASELEQIRSGKHNSGKWAGEGA AGCRREGERMEWTEMRGARGRRGGRER EMERARVRGGEEREKEIDLYKKVTSKIE ETKLGNNLLKLG
13598	27499	A	13755	175	21	KKKNFFFFPVRVILGPPKVFVKRAPLFFF FFFFFFFFFFFFFFFFLKKSWRPLAI
13599	27500	A	13757	234	341	ETGWVQWLPVPIPAVWEAEVGGLLLEPRS LRAARAI
13600	27501	A	13758	1	365	PAPNRRGGHIQDRATNSTELGANQCFFF SRPPSLEKKTPEINKEPRPAPQPSNPG NLGTREGGDSWAGTTRCLRRTDEGDTYR TEPPTALSWGQTRAFFFPALPAGKKRH RNLLKTQFF
13601	27502	A	13759	87	181	SHTHHTHTHTHTHTFYLVHVIHFDMEI LGL
13602	27503	A	13760	1	228	ARGERERERERERERERERERERERE RYREGGRLLLTMGEGETERATDLYHTPP PSIKAWRLCEPRPRAGILCGRNIF
13603	27504	A	13761	383	197	RCDPPAWVSQSARITGVSYRAQPATSVL MGEEDFLEDPVIAFVRLAPAVLLSKLSE VSVAMT
13604	27505	A	13762	276	57	YAVLGGGGGRKNLFVVFVFLFFFFFFFFF FKKQGFGLMPLGEDRGPNMGFFYPFPMVG DKTKLPFKKKKKRPR
13605	27506	A	13763	377	209	PRPAYGPAFLFTEGFSWNDFFFQMESR SVAQAGVQWCYLGSLQPPPPWFPGTLLN
13606	27507	A	13764	160	202	MEKYNVHPHSGILHSHEKEQAALFTIAK RWRQPSYPSIDEWKNIMSIHTVEYITAM KRKNQLYSQ
13607	27508	A	13765	390	284	ESGGHFLSLSLSIYIYIHIYIYVCYIY THTSHTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13608	27509	A	13766	350	41	YVILQENRNTQNRKLLPKSTELCMLLQ MLLFILNTTNYPLPLWQCYHRFCSFFLK TGSFYVTQAKVRWLTGMITVHCSLKL DSSHPPKWLVLQELATVAS
13609	27510	A	13767	330	156	KITQAWWCVHVVPDNRBAEVTGVIRLGR MRLPLEGACTNCVPSWEKEQDPVSHNEK K
13610	27511	A	13768	25	292	KCFFLSWRGGSRLQSQHFGRRPRADHLR PGVPDQPGQHGFLLVKMSDKPDLSEVEK FDRSKLKKTNTEEKNTLPSKEIFFSLVG VNIQD
13611	27512	A	13769	585	680	KCLGSRTRWLTVPVIPTLWBAEAGGSLRP RSS
13612	27513	A	13770	488	359	PSPRERKFLPFFKKKKKGWPPPPPKKNR GRGPQQKEGEPQKPKP
13613	27514	A	13771	794	515	PDMGLEDEQKMLTESGDPEEEEEEEEEL VDPLTTVREQCEQLEKCVKARERLELCD ERVSSRSHTEDCTEELDFLHARDHCV AHKLFNNLK
13614	27515	A	13772	130	397	VVGLTPLCFCMRASLPRHSPQARKTKK KKKKKKKKKKKKGGSLKKKIFGGAKKS GATKKKNFPKKRGQNKKNPGFFKNEIFF GGGAI
13615	27516	A	13773	376	145	TRVGGGCSEQRLCHCTPSWATEPNPVS NNKIPLELFPSNQTFHFVRNWKRGNN WLSNYSISSTVTRHFPFLFQF
13616	27517	A	13774	1	247	GLQSLADLLSGLLQKVCPLSNGIMDL LLYYLFTFTGSCSVAQARVQWCEHGSL QPHTSASSDPPTSATTCHHARLIW
13617	27518	A	13775	376	145	TRVGGGCSEQRLCHCTPSWATEPNPVS NNKIPLELFPSNQTFHFVRNWKRGNN WLSNYSISSTVTRHFPFLFQF
13618	27519	A	13776	107	468	EKARSPERARDQEGGTERDRNSEREKIL PKLREELPWVSGGWRCPPHQQGWSHWED NPGWGIPTGPSVGWGEKKGPGEGRSHKY GTGRTKCELGVSIGNSAFTLLHFYFKH RKRRKQI
13619	27520	A	13777	125	2	NIFFPLFELYFFKCHWARWLTVPVIALW EAKEGGSPEVRSS
13620	27521	A	13778	166	74	GRICYSHSLSKHTHTHTHTHTSHISF IP
13621	27522	A	13779	1	341	ARGERERERERERERERERERERERE RERERERERERERERERERERERERE RERERLSFSLGGGALKKKRIFLCVTL GKHLPLTHTGFFGENTHTLSMKTREGG FICAGGDERRSASVMRAYIYRECEPHTH V
13622	27523	A	13780	614	337	RRCSALCYRRHGNHVKIRSKQGASVS PHEHLRILSLEVRNVGLGHSIFPHSLR MYVCMYVCMYVCISYLSIYLSIYLSIY LSISISSR
13623	27524	A	13781	390	158	VLIRLSWGRICFQAHSGCWQNSGSCSHK TEGLCLLLAGSCSWLLGGALKGWASKEE FYTMQHSQSDTLSPLPYSIH
13624	27525	A	13782	308	163	TKFYLLFFFFFFFLFFFFFFFLKKKF LFFIQGGGKIKTPGTLTLFLG
13625	27526	A	13783	45	277	IASGRPFFFLHLPFPQAFVFGGGGGT PFEYQNFVAYIKGQGNPFLGCGDLFN

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						APQLIKQLSQLGQKYPKPKPLL
13626	27527	A	13784	413	218	PNFPFFLFFSGKFFFAONLPFGFFPPP GEGKAFPGQGCVPVGGGFAGPTFFFGPP AFPEILYFF
13627	27528	A	13785	1011	1368	IDWENDLTPMVLCHGPSIYNKYSFSQNI FPISANFFFLAHINLTLLQLVSELCHKI ILRHFYIKPIKDILNLYLILPGVWLPDL CKSTAICRYLCVCIYIHYIHTHTHIH YTHIRL
13628	27529	A	13786	161	425	RWGSCYCPGYPHLKIFKLLLLLVLEML GVLPLLPRLCSGMITVHCNLEFLGTSY PPISVSQTKKKRPFTLPPLPNLQICLP LRGE
13629	27530	A	13787	70	311	DLISITALVISPNKFYIYLSIYLSIYLS IYLSIIYLIFFISTNLLWVLSLWETLNKT RLNLFLTIQNNIWNPKLLVSALI
13630	27531	A	13788	25	219	RNMAAATLTSKLYSLFRTSTFALTII VGVMFFERAFDQGAIDYHVNCKLWK HIKHKYENK
13631	27532	A	13789	279	138	RRSLALSPRWDCGLQWRNLGSLQALLPG FTFFSCLSLFSSWDYRPF
13632	27533	A	13790	138	28	GGVVRWLTTPVIPALWEARVGGLLPEGSS KKERGGKEV
13633	27534	A	13791	133	7	YSCQRCLTHGQAQWLTTVISAPWEAKAG RLLEPRSVRS AWAT
13634	27535	A	13792	86	290	BHVHRTLIEASVSGWGWWLTPVISAAWE AEVGGSLGQEFELSLGKCSLTPSLTTT TTESLGSFAATS
13635	27536	A	13793	150	37	KTIYPSQARWLMVPVIALCEAEVGRILLE PSSSRLAWAV
13636	27537	A	13794	216	77	PTQHPTEGYMIKQQT VYHECRMWANS HL CLLPEGLRAVTPWCHAP
13637	27538	A	13795	251	347	VARAWGLAPVIPALWEAEVGGSPGGRSL KPAL
13638	27539	A	13797	177	274	VQWHMSVVPALQAEAEVGGSPGGRSLRPA WATY
13639	27540	A	13798	307	406	KFKKGWAWWLMVPVIALWEAKAGGSPES RSLRP
13640	27541	A	13799	194	3	FFFFFFFFFEMGSHYIVQARVQWLF TDA NIVHCSLQLLASSDPPVSTSQVGLQACA DDAQNP
13641	27542	A	13800	333	198	LPSVFFFFFFQTESCSVTQAGVEWCDLGS LHSSLGNRRLCLKIK
13642	27543	A	13801	1	335	ETERGRERETERGRERETERGRERETER GRERERERERERERERDRREGRRQRGE GKKNRDRENNRRRETERVGDVVCVCPHP NLILNCSPIYSHVLREGLGKTYLNYGGS FPTLCSG
13643	27544	A	13803	14	454	RVFFDRSRYSRTLGSTHASALLGILVY RSHLISSLLCLEGIILSLFIATLTILN THSLLANIVPIAILVFACEAAVGLALL VSKKKKKGAPVLKNPWGAQSLRGQARKY FFPYREPKNLPGNLGKEPFLGGDILG QPPYKN
13644	27545	A	13804	1474	1661	TDFHNSHLKCKNCIFSTLNYYIRREH FSIVFIFCYICVVKVHYIRRELFRCLYF LLYMCC
13645	27546	A	13805	360	3	LWCKRGPPFSPPPFFFLFLFFFLKMG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion; \=possible nucleotide insertion)
						GGGFFGGFPWGPCKGEIFFFVFFWAPQK KKKKKPPPFIFWGGGPPFFFFFPKQK KKKNKKKKKKKQKKKKKKKKRAARWPA RSRSSA
13646	27547	A	13806	1	425	RLGGVALRSAADGAFVSGEF CGGKLLRW CLVTDFFPDSCTTCSYSRRSTPGCSPGG SRGLSEGE GSSVSLQSRVLSAMKHVLN LYLLGVVLTLISIFVRVMESLEGLLESP SPGTSWTTRS QLANTEPTKGLPDHPSRS M
13647	27548	A	13807	5	313	EKPYLQGITFTSKTTHLIYEFTPYTIIV KEYSTNYVLLIGNTQITKIYHIVFRKFS MTPIYKFQDLAQWLTPIPTLWEAKPGG LLEPRSLQSSYSLLIILIL
13648	27549	A	13808	182	314	VITQLDKTERAQWLMFVILVLYEAEVGG LLEAMSSRP AWATKTW
13649	27550	A	13809	219	1812	LPPPESGAMSGFNFGGTGAPTGGFTFGT AKTATTTT PATGFSFSTSGTGGFNFGAPF QPATSTPSTGLFSLATQTPATQTTGTF GTATLASGGTGFFLGIGASKNLNSNTAA TPAMANPSGFGLGSSNLTAISSVTSS QGTAPTGFVFGPSTTSVAPATTSGGFSF TGGSTAQPSGFNIGSAGNSAQPTAPATL PLTPATPAATTAGATQPAAPTPTATITS TGPSLFASIATAPTSSATTGLSLCTPVT TAGAPTAGTQGFSLKAPGAASGTSTTS TAATATATTTSSSTTG FALNLKPLAPA GIPSN TAAAVTAPPGPGAAAGAAASSAM TYAQLES LINKWSLELEDQERHFLQQAT QVNAWDRTLIENGEKITSLHREVEKVKL DQKRLDQELDFILSQKLELDLLSPLEE LVKEQSGT IYLQHADEEREKTYKLAENI DAQLKRMAQDLKDIIHLNTSGAPADTS DPLQQICKILNAHMDSLQWIDQNSALLQ RKVEEVTKVCEGRRKEQERSFRITFD
13650	27551	A	13810	134	263	KNSLFKKKNNGRPWPLMFVIPALWEAEA GGLEPRGLRPTWVT
13651	27552	A	13811	210	51	TLSHRKPISEAYFARVRGFILEVSETR NPPIGWTRWLTPIVIPALWEAEAGG
13652	27553	A	13812	241	139	LHEAGLAPMIPALWEVKVGGLLEPRSPR PAWASW
13653	27554	A	13813	539	256	RTTQMSTAAGFTEAPNWKQPRCPWTTEE TNKMWSLHAMECASAMKWEVL IQPAVR MARENSRRKPGMDHDIWSVWSAGEWLP LGRSTGKGS
13654	27555	A	13815	63	369	VRETPLKTHYLEEISSPASPTAIPQSL FSFFISPPSSLATGSGHSGHPVHSLHHP PETEPSVSVCLWAGPKVPPGAAGKGS PD SNPLVIRSLAPPASL
13655	27556	A	13817	258	3	AESAPPFSTNSLFFTHTHTHTHTHTH THSLRTRWAPSQVCRPQTSQRGECVG PTAFAPSPTLLKPHHPSSHVHLP SQPRR
13656	27557	A	13818	516	665	WFKSGSFWLGMVAHTCNPSTLGGQGGWI TSGRSRTSVTTTTTSQT CAPA
13657	27558	A	13819	295	361	WLTPIVIPALLEAVTGGSLPR
13658	27559	A	13820	166	368	GWATQHS AQYVVSSSSGTALCLGESCS VTQAGVQWCDLSSPQSPHPGFRFLCLS LPSSWDHRGDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13659	27560	A	13821	133	530	RKYCGQCLNMLNNVSLSSGDQSRVAY RSSHGDLRPRASALAMVSGDGLVSRPE AIHLGPRQAVRPSVRAESRRVDGGGRSP REFDGRGRSRQARFSPYPPIPAVEPDLLR SVLQQRLLIALGGVIAARISV
13660	27561	A	13822	76	1958	RQELIWPLCSPPQGDRLQKSWIFFRPV MADKLTRIAIVNHDCKPKKCRQECKKS CPVVRMGKLCIEVTPOSKIAWISLCTI GCGICIKKCPFGALSIVNLPSNLEKET HRYCANAFKLHRLPIPRPGEVLGLVGTN GIGKSTALKILAGKQKPNLGKYDDPPDW QELITYFRGSELQNYFTKILEDDLKAI KPQYVDQIPKAAKGTVGSIIDRKDETKT QAIVCQQLDLTHLKERNVEDLSGGELQR FACAVVCIQKADIFMDEPSSYLDVKQR LKAATITIRSLINPDRIIVVEHDLSDLD YLSDFICCLYGVPSAYGVVTPPFSVREG INIFLDGYVPTENLRFRDASLVFKVAET ANEEEVKKCMYKYPGMKKMGFEFLAI VAGEFTDSEIMVMLGENGTGKTTFIRML AGRLKPDEGGEVPLNVSYKPKISPKS TGSVRQLLHEKIRDAYTHPQFVTDVMKP LQIENIIDQEVQTLSSGELQORVALALCL GKPADVYLIDEPSAYLDSEQRLMAARVV KRFIHLAKKTAFFVEHDFIMATYIADR IVFDGVPSKNTVANSPQTLLAGMNKFLS QLEITFRDPNNYRPRINKLNSIKDVEQ KKSGNYFFLDD
13661	27562	A	13823	3	292	KCWDYVHEPPRPAPMQTYQVDLRCCFVS TINLLVCGERASLPSVESLVFSGLAEBVW MKAVLAPSRESGKLVLQQVPEYAEAIWG ARPAACRGLVFSA
13662	27563	A	13824	245	91	YKVNFGPPRGSGFFRPPPPFFFEVHFHFF IIFFFFFFFFSSFFLGCFFMYV
13663	27564	A	13825	276	100	PGQKKKTLSPKKKSIYLYIHTHIYIYT HTHIYKYIFVCVYICVSIYIHTHIVPR IFS
13664	27565	A	13826	202	375	IYNTYIHTHTHTHTHTNVLYIQSGDC IYAVLLGELSFIYIFVFLSSLISILPHL TY
13665	27566	A	13827	278	34	KPRGLSPAGVSAQRAWGPHSCPLPDPR TELQVRQIPALVGSSAFQGRGRKGPVG GSGPSRPRAPPQPRPGCCQCTLLQI
13666	27567	A	13828	62	307	GCARATFLNVPHLKRPMFFLELCLSTKC PVGTEFALDSLRLYNSNTFCWVQWLMP TIPALCKAEMGGLLEARSIPAWAT
13667	27568	A	13829	386	478	NRIGMVSHACNPSTLGGQRRIMRSGDQ DHS
13668	27569	A	13830	364	484	NFNILGWAWWLMPPVLPALWEAKAGGSL EVRGSGPAANMV
13669	27570	A	13831	33	486	PARSAEFGTRERERERERERERERERE RERERERERERERERERERERERERG VICVCPCALLCVRESDFLSQKKYCVCFV VVRYTESLALSPFCLGRCLALLIFLEGM WRKIWAPSLSLCVGALFFSQHPPPFWC LCVLSLVRPLPLSLSGGVFVSQRALI
13670	27571	A	13832	6	718	YSAVEFAMAGVGAGPLRAMGRQALLLA LCATGAQGLYFHIGETEKRCFIEEIPDE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TMVIGNYRTQMWDKQKEVFLPSTPGLGM HVEVKDPDGKMLQVVLRSQYQSEGRFTF TSHTPGDHQICLHSNSTRMALFAGGKLR VHLDIQVGEHANNYPETAAKDKLTELOL RARQLLDQVEQIQKEQDYQRYREERFRL TSESTNQRLVWWSIAQTVILILTGIWQM RHLKSFFFEAKKLV
13671	27572	A	13833	17	130	RLQEFGRTRERERERERERERERERE RDTHSFLHG
13672	27573	A	13834	283	460	LVVRLAICKNYSKRETEPGSVAHVYNP STLGGQGGRTARGQEFKTSLDNIARPPS LQK
13673	27574	A	13835	3	435	WPRFCTALQEFGRTRERERERERERE RERERERERERERERERATSLSRARPSF LFPSACVSHTPYVGERENLSLHTLKH TREKHSLSYTNASARDTRARFSEGRAPP IYSVYLTHGVFFFFFFSLCLSVRHAEGL AHV
13674	27575	A	13837	351	57	RTLHVHISKFTGNLSDLYVQSEWQDLGT ADLSIMTSVLHCLPSLESIKNTDSWPSS VAHTCNPSTLGGRGRCRDQHGQHSKQPS LLKIQKIARRCGG
13675	27576	A	13838	336	150	TFCYKKYLWGAHCFIFRTTGLPIKNFYF GQAWCLLPVISARWEATEGGSLEPRSLR VAWAS
13676	27577	A	13839	310	454	HCSLGLPQVLLIILYKILLGWARWLT IPALWEVEAGGLLEARSSRP
13677	27578	A	13840	163	297	IIFFLDLKLQGAMTIVVSIYLSIYLSI YLSIYLYTHLTWNTLQL
13678	27579	A	13841	33	316	LDQHPTPRSPLLCHSLRKTSSSQGGKSE LVKQSLKKPKLPEGRFDAPEDSHLEKEP LEKFPDDVNPVTKEKGGPRGPEPTRYGD WERKGRCIDF
13679	27580	A	13842	4474	2586	DGGSGCVKMEFPGGNDNYLTITGPSPHF LSGAETFTHTPSLGDEEFIPPISLSDSDP SLAVSDVVGHFDDLADPSSSQDGSFSAQ YGVQTLDMPVGMTHGLMEQGGGLLSGGL TMDLDHSIGTQYSANPPVTIDVPMTDMT SGLMGHSQTLTIDQSELSSQLGLSLGGG TILPPAQSPEDRLSTTPSPTSSSLHEDGV EDFRRQLPSQKTVVVEAGKKQKAPKKRK KKDPNEPQKPVSAAYLFFRDTQAAIKGQ NPNATFGEVSKIVASMWDSLGEQKQIY KRKTEAAKKEYLKALAAKYKDNQECQATV ETVELDPAPPSQTPSPPPMATVDPASPA PASIEPPALSPSIVVNSTLSSYVANQAS SGAGGQPNITKLIITKQMLPSSITMSQG GMVTVIPATVVTSRGLQLGQTSTATIQP SQQAQIVTRSVLQAAAAAAAAAASMLPP PRLQPPPLQMQPQPPTQQQVTLQQPPP LQAMQQPPQKVRINLQQQPPPLQIKSV PLPTLKMQTTLVPPTVESSPERPMNNSP EAHTVEAPSPETICEMITDVVPEVESPS QMDVELVSGSPVALSPQPRCVRSGCENP PIVSKDWDNEYCSNECVVKHCRDVFLAW VASRNSNTVVFVK
13680	27581	A	13843	54	251	EFYRMNSPSPLWLCVCVCACLFMCLC ALTCMCVWYKSLLSNLTVLSSKPYDS

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SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13701	27602	A	13867	161	304	LFTAEMTSHYIAQAGLELLASSNPPTSA SERTGITDGGATEILPQLRL
13702	27603	A	13868	230	348	VSFQNLVFCVERVYRVPDFGVWVERGSK YNNGSTELHSK
13703	27604	A	13869	168	260	EVIAECYNGCFQTLSLCVCVCVCVCVCV CY
13704	27605	A	13870	140	16	LKYGQWRDLGSLQPPPPRFKQFSCLSLL SSRNCTTMRDHE
13705	27606	A	13871	143	30	KILKVVVSQAWWLIPVIPALWEAEVGG LEPRISRLA
13706	27607	A	13872	158	59	HLHGCIHLLKLRLDAVSHACNSSTLGGQ GGRIA
13707	27608	A	13873	232	115	APFFFKGAPIFFFFFFFFFFFFFFFFLIR GKPGNDVGVGEG
13708	27609	A	13874	1619	1375	KTWRRHLEKLQDMSLLRHRVHVDSSQG LFPFFQRRQLLPRLKCNGLIIPYCNLKL LGWSNPPASAFRVARTTSLCRHTWL
13709	27610	A	13875	219	84	NPLQSTSTICNRAWDRVTCWSQLLRRL RWEDHLSFGVPSCSAL
13710	27611	A	13876	166	496	KKKKKKKKGGGGLKKTGGAKINRGRK KKIFFQKGGQKKTGGILKKPFLGGGK KGNPPKKIKGLREKKKFKRGKAKPAQ NPWGKKISPPGFLLKFFPRGRGFFI
13711	27612	A	13877	132	348	PSKKKKRGGPFKRTPGGPKFNGGGKGN FPLMGGGIKPNLGLGNPYLGGGTNGN NPPTIIGFGEKKKF
13712	27613	A	13878	287	134	QQGPPISPGPKENRMGPPSPGWGNGPI RSPPGAGPNPGAFQDGMFSPKKQ
13713	27614	A	13879	333	480	VHPLRSAEGPRPESNMLHLLKSKQQWL TPVIPALWEAKAGGSQGEIE
13714	27615	A	13880	1	227	PKIHCKIQHIVVLVSFFPSFFLSFFQGE SCSAAQAGVQWHDLSLQAPPFGFKWFR FIELLGLGFHSRRMRGKDS
13715	27616	A	13881	276	378	GWPWWLTPVIPALLEAEVGGLEPRSLR LALAT
13716	27617	A	13882	126	389	GSVLGTGCCSVLGTVCGRSVLGTVLIA SATPDRYLRLSSGSSLTRITNSDLVPWL TPVIPALWEAEAGVSLEPRIWRPARETW EDPH
13717	27618	A	13883	414	150	ARQAPKWGNPTGSPPPGFLNPPPKNFFL GPQKKKIFFPTPPPHFFFKGPPPPFF FFFFFFFFSPHAGSILLCHPGRIAVASW LTE
13718	27619	A	13884	197	363	DLGVVVNTFMLKFKCLNVSRGHVQWLI IPVIPILWKAZAGRSCLKPRSLRPAT
13719	27620	A	13885	101	236	NIHYANFPYFGLACPEYIVRALQKKYTQ THHTHTHTHTTRTTTSL
13720	27621	A	13887	17	140	TVHLKMKVIGLHMVAHACNPSTLGGRG PIMRSGALGNFCL
13721	27622	A	13888	135	1	VLHAGLKLGSSTSPTSASKGAGTVGIH YHTQLAFQFFLFCFLIR
13722	27623	A	13889	411	276	TLYFKHGMGFHHVQAGLELLASSDPP ALEFETSLHNKVRPRL
13723	27624	A	13890	216	54	EFKLCYTLFDHSYFPLEELVSGQVWRLR PAIPSFWEAKEGGSLPRSSKHEIV
13724	27625	A	13891	3	149	SSDPRPSSSWLAWVGLWSMVVRVPPFL PILFLASHVGKSPSPSPHF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13725	27626	A	13892	166	1	LFSKIFWWLLPVIPALREAKVGELLEPGSSRPAAWATWKNPVYTKNTKISQAWQCT
13726	27627	A	13893	128	2	FSTTYPNPIKLPHPYLPPLTLFLDSAHLHPSEINSLVAQKKK
13727	27628	A	13894	225	391	HLSEIHILTFPFSLEQWLVPIIPVLWEVKMGGLLEPRSSRPAAWATQDPQVSRK
13728	27629	A	13895	192	1	TLVCVSSSVPKYNNICLACWFMPIIPA LWEVESGSLLELKSSPPAWPTWWVPLKS KNTKISLA
13729	27630	A	13896	152	245	DQSIADVLMYYTHTHTHTHTHTHTLQNVPG
13730	27631	A	13897	270	406	ISTRFFLYRDRASLCHPGWSAGVQSWLPGSSNSQAQAILLPQPPE
13731	27632	A	13898	232	73	EAEGPRDVTSSTFHWRLYDQTTNYHECRMWANSRLRLTPEGLLKVITPWCHAH
13732	27633	A	13899	107	7	LGQAQWLMPTIIPALWEAKAGGSLEPRTSRPAWA
13733	27634	A	13900	62	224	PTRPILAHCNLCVLGSDDPASASQSAGVTGMSHCAWSNLIHLPSRSTAICTL
13734	27635	A	13901	450	194	KRQVKSHSEVKTHVQWPGIDPGSPAWEARILPLNHQRLSGTTPWRITEKSNHKDL ETVLSGFFKCRCLKANKDIQTKCVFIGNF Y
13735	27636	A	13902	300	404	AAPGRAPQKKKKKKKKKKKKKKKKKKKAPFIKRGR
13736	27637	A	13903	131	29	ALGSLQPLSPRFKRFSCLSLPSSWNSTALTVTTM
13737	27638	A	13904	267	74	VWVLVPPFTSYGVLDKPIIVNNIYVHV CVCLCMVCVCVCCTVIRRHCHWHNMI IIISQHDQ
13738	27639	A	13905	193	64	IRSHQIHKLHFKKFRILGWTWWLTPVIPAPWEAEGRSPEPSS
13739	27640	A	13906	309	424	QSTDLENRRVGGAWWLTPVIPALWEAEVGGLPEIKNS
13740	27641	A	13907	404	251	SCLISLRSDYRHVPPQANFVFFFEM ECSVAQSGVQWQEENSISKINK
13741	27642	A	13908	471	59	GPPQAKKGKGFPTPGPPQKGGGQPKSG VLGFSPPLGCPGLGPPKGWGFWGGSF FFFFFRKWEHKNELFPFSKTEKPRRAG EARKGSQSTKYAGLSRGERQASPTLRPG HLAKASAGGWLQYTRWQGLPEPGN
13742	27643	A	13909	479	231	QBYCMLIFCEHFGDFDLNIVFCLEKMKVGVIADFYLLSSFTGRPQWLMPVIPTLWE AEVGSLEAKSFTPAWATWQDPISMF
13743	27644	A	13910	167	19	CIVLGIMLDSLWEPRQWVPSVWRWFTPVIPALWEAEAGGSPEVRSSNS
13744	27645	A	13911	328	446	GSFSKITDLSQTWWYVPVIALQSEVGRSLEPRSSRLQ
13745	27646	A	13912	145	460	NAFMSTGCEVLSYSELQRNLVWVFLPVIPATPQAEAGRLGPRSSRPWATKGVRALSHKQTNKTKNLSHSTGVSVFTHIHSPGILWRLSQWLLAMNLATN
13746	27647	A	13913	319	210	KLGFEEKGPPLEFFFFFFFFFFFYGFLT TVSCNFTL
13747	27648	A	13914	372	10	PNTTCTPITYGKKCCPREISYYLCHEFT RIRILTFDGEDSCYIAQAGLKLGRSP PTSASGVAGNTDVCHHTQPIIFYILETG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LALLPRLILNSWSQAILLPQPLRSYFNFWLFFCLYN
13748	27649	A	13915	594	471	PSYIAYMCICMCVCVYVYINICVCIYTHVHTPYNPVISKN
13749	27650	A	13916	235	3	EANNLIRKTYTSGWFQRTSKRPPAVRRMKVLEFFETESCSVAPVGVVHDSLLQPRPPGLNRSSHLSPSSSDYRWA
13750	27651	A	13917	272	184	KTTAWAQWLTPTVISTLWEAKVGGSLAEGS
13751	27652	A	13918	46	321	SRVQGTGGHRGRGCIQACVGEQEAQRET EGGPWRWLTPVISKLWEAKAGGSLEPVSRRATWNLLKRIYYTDEREYLIPLALNTSQGSTFSF
13752	27653	A	13919	387	484	FTEIIGWARWLMPTVPTLWEAEAGGSPEVRSS
13753	27654	A	13920	142	321	FLFSIHFLHSCWGLFSNVQSLSIFSLSYLVRLYGQAWWFTPIILALWEDKAGGSLDPRSL
13754	27655	A	13921	270	412	IEDKKIYSILHTETLERQCARWLTPVIPAFWEVKAGGSFEPRLRPV
13755	27656	A	13922	304	396	NFGWAQWLTPTVIPALWESEAGGSLEPRGLRS
13756	27657	A	13923	305	387	VWWTPTVIPALWEAEAGGSPEPRSSRP
13757	27658	A	13924	103	3	NKSPELGWAWLAPVIPALWEAEAGGSP EVRSS
13758	27659	A	13925	195	400	CLLILSGLVASCIERHGKGQAWWLMPTVPTLWEAKVGGSLRLNRLRSAGTWRNSISIKYTEQLAQG
13759	27660	A	13926	294	489	KWAKMQTLHKGRYACVCICVCVCVCVYT YTDIYIFYIHIWPMNTKCSMLLVIGEMKILSRMWSNQ
13760	27661	A	13927	363	2	NWGPPGFPFPPFLKTGPVFFIFGAPKKK FFLSTPRALKFVLLKGGPLFFFFFLVWFLVKTGSHCVAQPDLELLSSNPVLVSQ GAGITGMSPQVQPLDLFFFSFFETGSR SYAWADAN
13761	27662	A	13928	1	218	LRPFKKRKTNPKMWSVHTMEYHSALKRKBIRTQTTRWINLEDIVLSEIRVAVTKGRILYDSTQMRNLEESNL
13762	27663	A	13929	219	408	TFCHFIAFLHVKMFVVFVFFSFIMFFFP LNCNKAERKKKKKNNKKKKKKRKKISLSPPAPP
13763	27664	A	13930	161	22	WHPPASASHVAGTTGACHHERLRQEDHFSLRVQGCSEPRLCCHHTPP
13764	27665	A	13931	116	1	INTGWARWLTPVIPAFWEAAVGGSLPRSTSQAATWK
13765	27666	A	13932	181	38	PWPQRATQPKISPLPPAISALWEAEAGG ALEPRSSRPAAKSDAWVD
13766	27667	A	13933	267	397	TVFDRTLFFIKKIHSWAPWLTPVVPALWEAEVCGSPEVRSSG
13767	27668	A	13934	129	12	NIGVGWALWLTSPVLPALWEAEAGGPPKV RSSRTARPMS
13768	27669	A	13935	179	1	KTYYGGIPIPPGPPKKGEKKPPFFFKKFFLFFISFFIFFFFFFLRLQSLAKMQSASVW KVS
13769	27670	A	13936	245	616	DDKKKKEAAQKKATEQKIKVPEQIKPSV SQPQPANSNNGTSTATSTNNNAKRATAN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NQQPQQQQQQQQPQQQQPQQQPQPQPQQ QQPQQQPQALPRYPREVPPRFRHQEHKQ LLKRGQHFPVEF
13770	27671	A	13937	121	292	NTDLDLALALIVRVLTSDDNFKNKGWVQ WLMPVFPAPWEAEVGSSEATNLRPAWA T
13771	27672	A	13938	421	202	GPREAPLFPSTQGISRPLFFFFFFETES RTVTRAAQWHNLGSPQPPLCSLDILKT SQSVCMPAEAILVSQIT
13772	27673	A	13939	205	543	ILESRRRLGWSEALPENQLLCRASSWES LGPPDPCLKPPSPAFWGAAGGWRAKST SVSEPVVGTLLVALFLEMAVGLLLGLP FCFHSGLGAPHLLECPDGPVLPAEARQS R
13773	27674	A	13940	140	2	LSQHSEETLPPPLYLEKESRRPPPPQH TPHPPPPWPWHPDIADIQ
13774	27675	A	13941	47	303	GLIFLIITWTCIVKTSTDFPRMEDCSQCI HQVTEESNKRMGFLSYIANPHHGSSRL WPQHAAPWDDGRRGKPVFSLGFVSFPFP Q
13775	27676	A	13942	1488	1719	PLVSFSKNTYPCLGNVKNQKTTFCSRW KLHVLSSNLSSPAEVTVASINLVVSEQ SFQNSQLPAMLCILVHLQMS
13776	27677	A	13943	127	402	QVTHPPNRTMCSSMIFFLYLCLFLSL PFPSHLSLYAPPKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKAGGGGPFK KKIHFPGGGRIIFY
13777	27678	A	13944	852	209	EQTVYCTRIDLQKKLVFLLEAFCLLSQ GDPGSPMMCQLQQFDLWVLRGVNFGGE TCPGLFLYTKVEDYSKWITSKAERAGPP LSSLHHWEKLISFSHHGNATMTQKTY DSELGHVGSYLQGGRTITHSRLGNSSR DSL DVREKDVKESGRSPASVQPLYDY YGGVEGEGRI FAGQNRLYQPEEILGSL RACFLFAAVSSPGATPPN
13778	27679	A	13945	68	260	INIFWHCVLLYVILYAISQFLFPCKVN IASWLGSAHACNPSTLGGQAGESLEPR NLRPAWAT
13779	27680	A	13946	420	156	FLPPGVKYGSFKRAPPPFFFFFFFLVET LSCYIAHTGLELPDSSNYPTSASQSAVI TGMSHHTWPLEGACLAIPQALRILLVLV PLH
13780	27681	A	13947	317	17	AGHGGSTCNPSQPIVTAVPINLWGRDLL QQWGAQAFIPEQLYSPQSQHTMQEMGYV PGMGLEKNLKGKLPQAEQGNSHQGLG YNFSWQPLLSLQNL
13781	27682	A	13948	55	224	NFRLTSSFSYLKMSFWLGMWLTVPVIAL WEAKTGGLFEARSRLVWVWQSKKAGSHL
13782	27683	A	13949	1464	805	RATSVRGAGRERSCGAAWSPASIGPFLR RSVLPNAHFRSSREGGMAASTDMAGLEE SFRKFAIHGDPKASGQEMNGKNWAKLCK DCKVADGKSVTGTVDIVFSKVKGKSAR VINYEFPKALEELATKRFKGSKEEAF DAICQLVAGKEPANVGVTAKTGGAVDR LTDTSRYTGSHKERFDESGKGKGIAGRQ DILDDSGYVSAYKNAGTYDAKVKK
13783	27684	A	13950	356	98	NAGPGIYFWGPICKTLPCPPAGVKLGSL KRAPLFFFFVEMGFHHVAQAGLKLSSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DSPIPVQSIRITSTCEPPCLAKIKSSLRL
13784	27685	A	13951	194	48	NFLEGWPGQRLTPVIPALWKAEEAGGSLEPKTFRPVWAMWRDRLRKPQH
13785	27686	A	13952	341	418	DQPGQHGETPSILKIQKLAGRGSTCL
13786	27687	A	13953	158	323	TWLKKYFQSTNQLPPAHLNVPQLLPFGLEPLLPLKKKKKKKKKKKKKKKKKK
13787	27688	A	13954	231	355	VFLPQKQKQNCPLTGKWNNSWNIHTLEYYSAVKGMKQLI
13788	27689	A	13955	493	39	PAAFSSSWGAPGSSLLKKTTPASWPPGLLEPPAPVSSMAAPDLDSFPLPLCWTFRLVLCRVFSSSTLAFLSCVSTSFALTTPAASSNIFSIISLPHWASPPLPTARLTSVSPPELPLPLPSRLQRQPRGAPSHPGMSMGPIILDATSNSTTSR
13789	27690	A	13956	497	372	NTKISWASWYAPVIPATWEVNSNRPAIHSHQPPKRIGLQA
13790	27691	A	13957	438	301	GTTYLDIDMTCDYVSVCLCIYICTRQQSYIYTYVYTHTHTHMYI
13791	27692	A	13958	84	466	QPLGRSGKVPQLHLWEMQRLPAAFFRSFAAQGLGESVHINTPTSLSLRGRPFISSSGPGARARVTCAPCLHAARILCCFWRLHRLKCSNVISAHCNLRFSGSSDSPASASQVAGITGRSSLEQLLE
13792	27693	A	13959	216	28	KYVKNYVLSSIFWMQEIFHNFKKSSRTQWLTPVIPALWEAEAGGSPEPRSSRPASSIQLENS
13793	27694	A	13960	320	943	VLSFSLSDRAQRNCNRMGKQNSKLAPDEV MEDLVKSTEFNEHELKQWYKGLKDCPSGRNLNEEFQQLYVKFFPYGDASKFAQHA FRTFDKNGDGTIDFREICALSITSRGSFEQKLNWAFNMYDLDDGDKITRVEMLIEAIYKMGTVIMMKMNEEDGLTPEQRVDKIFSKMDKNKDDQITLDEFKEAAKSDPSIVLLLQCDIQK
13794	27695	A	13961	191	8	GLFRFRRLSEEVKHCCCCCCCCCCCCCCCCCCCCCCCCCYLRLAPQSPAAPAPELHTPLPGSRNR
13795	27696	A	13962	203	28	VWGNQHFCFVPVFRKKVFCFFPLNKLRLGGGFFFFFFFFFLVFIDNSWVFLGEGDLA GS
13796	27697	A	13963	18	171	GIRHEERERERERERERERERERERERH PAREIDMCVSKRDTRGALCALF
13797	27698	A	13964	25	299	HDFCTRRERERERERERERERERERERE RERERERERERERERERERERERE RERERERERERERERETHLSLYIMCVFLYIPLYFSFLYIHTQREAPPPLSATLSLSIL
13798	27699	A	13965	246	410	AYNGQSGRGVTPVIPSLWEAKTGGSLERP RSWRSAWATWHTPPVPGSKEISLYI
13799	27700	A	13966	91	26	FCCCGCCCCCFYCKKEKTLV
13800	27701	A	13967	158	24	PFCHIIYIFLESFVAMLECSGKILAHCYLRLLGSSNSLVPSLA
13801	27702	A	13968	129	7	SWAQWLMPIIPTLWEHEAGRSLEAMSSRPAWATQQDPVSKK
13802	27703	A	13969	445	268	KIQLTKLKNASESLPSRINQAEKISGWAWCLMPVIPVLWEAKAGGSLEPRSLRRGQVT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13803	27704	A	13970	1628	1309	HRRKKCAGYSSLSALLRERERERERERERESVVCVCLGTITCFRRQYCVIQGI SGVRQNCVQIPALSDPDLFLFLSLSVLH SNTWVVRPTLRVTERNKGAMCV
13804	27705	A	13971	314	140	QCHNCYILTLQLVKIKGDQAWLMPITIPA LGAKAGGSLEAGSLRSAWATWRAPMSTK IF
13805	27706	A	13972	292	482	YKSVRTQDSCAHGVDRLVGKIRYVNL FV YICQHS DGRTWWLTPVIPPLWETKGGGS SEVGRSG
13806	27707	A	13973	502	303	STAIGPSFSFPFLCTHGSFHGFLFFFFCF CFFLVEMGSHYVAPAGLKLGLSSDPPAS ASPSHLGLQV
13807	27708	A	13974	493	289	IPPTALGTSTSPFLCTHGSFHGFLFFFF CFCFFLVEMGSHYVAPAGLKLGLSSDPP ASASPSHLGLQV
13808	27709	A	13975	405	121	IREAAQSESLFVRAAPHTGLISGPCITE IYAVKDTRCMQRRILVRELECAAHGLTE CLSIDTHTHTHTHTHTHTHTHTHTHT HTGRWEAGQSLKGES
13809	27710	A	13976	135	254	TVTCTNSSWSLTFTSFLFLMPGWIQGR RVCVCVCVCV
13810	27711	A	13977	179	58	VPLSINSPQRQCI FCCCCCCCCFLVLQ KIISERSWAEIG
13811	27712	A	13978	97	186	KIIFWLGVVAHACNPSTLGGQGGRIMRG RD
13812	27713	A	13979	289	420	ELGLKIHGFPSQAPWFMPIIPALWEAEA GGLLESRSSRIAWAMW
13813	27714	A	13980	421	106	SGGRNFFFFLGGGFYKKKFP PPPFLRGK KKKPPLPKKKNP TIFPPPGGGPPFSP PPKGGGKIFFFFGKNFIMQNF GGFPL WGKKKKFLPKKKNPL FFFFFFF
13814	27715	A	13981	309	135	KHIYIYLSIYLSIYLSIYLSIYLPAYLP TYLHAHPLIHANAYKNIHIDYPFKKGFE Y
13815	27716	A	13982	231	21	QHMYCLKSIWHKKLSRKPYCIISEYSS MVKLRVSISQVQWLMFPVIPALWEAKAGG LLKARSSRPMWAI
13816	27717	A	13983	209	359	HLHTHTHTHTPNGVKQIMTQIPILPLTG PLILEKFLNFSKPLSHPGKRD
13817	27718	A	13984	391	249	IWPILPPQKIF FFF FETESCSVTQARVQ WCNLGLSLQPPNPVFP SLAK
13818	27719	A	13985	181	403	YLVLDSPESHATLGILSQPKDYITKDQTLT FRPVVVAHACNPSTLGSQK WITSVQEV ETS LCNTARPCLYQKYKN
13819	27720	A	13986	441	358	ETGSR CVILAGAQWRDLSSVQPLPPRFK
13820	27721	A	13987	7	233	ASIPCIYQKTKIPNTKQTKNKNTKITPA WWCTPIAPATQKAEIPPLHSSSLGDFLRL SPKKKKGGPNWAPT SKFF
13821	27722	A	13988	152	44	PKAPL FFFFFFF FFF YETRSHSVAQAKV QRHDHGSL
13822	27723	A	13989	188	379	NVSCHA AETRVWWEKERPLVPF GAYLL DGMPLVWLLSASSILSIWLSIYLSIYLS IYLSIYF
13823	27724	A	13991	296	53	SSILFHASKYHFSGRLFSLLSCKRRN I LQLVPHMYSPLYMYIHTHKHIYEYMVH IYIYMNL RNCRIY LHSCTPKENQAR
13824	27725	A	13992	37	290	RLGSPASRHHQQIQCLIRACLKDGTLGWV

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						WWLIPVIPALWEAKVGGSLPRSSTPAW ATQGDLLKKDGTLLQCPHVAKGHSSHS
13825	27726	A	13993	189	370	SRNAIFKKRWESSCQSSFNLSGVFPQAA TKGWVRWLTLPALWEAKAGGSLPRSS SRPA
13826	27727	A	13994	179	25	SKHNKKNIQICLLCSKRSMFVHVCIIHI ICVYVYRYAYIYIGMCIHIYIHS
13827	27728	A	13995	159	2	EDPLSPGVQDQHGHRKSLSGRGKISL GQEFKSSMAAMYFGRSGGCKLERR
13828	27729	A	13996	307	99	FIWEHFVNYTMFFTYKKPTSQANWLMFV VPALWETEAGGSPEVRSRPPGQHDDVR PLGPSLHVYLQMD
13829	27730	A	13997	218	21	FQHFGRPRRVDHLSLGVQDQPGQHGETP SPLASSILDLI PPPFIDE PVDLAFQSV TLGVQDTTS
13830	27731	A	13998	227	404	GYSVTLLGLTQLTQRIAHGTRKGERER ERERERERERVCSCLMHELASHLLFFFL FRE
13831	27732	A	13999	400	668	PVGRRWELQGMGLGVRTWQSSLPQCQPT SSSVLSLGRGTPGISNTCLPPRSATELG LPAQVPFPNVQSQDQLSFLGCFPRTY NRQTL
13832	27733	A	14000	225	414	NRVLLCHTGWSTVAILAYCSFKLLGSRD SPTLASRAARTIVKCRNVWLIKKKKKK KGGRRLL
13833	27734	A	14001	397	118	LFSGPFFFDKSECFQEPFVFCLLLYNQ MQPYLLRSFAVDSYYMDSFLDRVVSFC QSGWSTVAPSRLLTAALNSLAQVILLPQP LNVLCGISR
13834	27735	A	14002	3	173	YVFYRQKQMVCFYKIRIKNMFNRRLNL GQWCVPVPATQVAEAGGSPEPTSLRPI
13835	27736	A	14003	440	290	YHTLYIYIYIHTHTHTYIYLCTYWG QFDLLVLDNKLYKEIYLSVFI
13836	27737	A	14004	2	116	ARLVAMPFKYEETKDFLLTARRKDAKSV KIKKNKSAAV
13837	27738	A	14005	279	422	SAKAPLSCLRTNSLLKNGLRGWAWWIT PVIPTLWEAEVGGSPDVTSP
13838	27739	A	14006	3	497	GGIGDSRCGSTRASSPQLAGRSSSVLP AAAQPCPTPMDVFKKGFSTAKEGVVGAV EKTKQGVTEAAEKTKEGVMYVGAKTKEN VVQSVTSVAEKTKEQANAVSEAVSSVN TVATKTVEEAENIAVTSGVVRKEDLRPS APQGEASKEKEEVAEEAQSGGD
13839	27740	A	14007	1	292	SLGGGGCNDPRSYHCTPAWATEQDTVSL SLSIYMSVRVCIYMYMCVCVCIRIYTYI HTHIHIRVYIYTIPIYIWIYIYIYVDLV IYMGWCGCPPPSI
13840	27741	A	14008	57	250	KIFFFLMNTWGGVPVVLATWEAEVGG LEPRSLGLQETMMTSLSLRPPRQGEIL SLILKRN
13841	27742	A	14009	184	2	AVPGRWPCQQVPGLLPSIQDTLKQGRGTG QWLTPVTPMPWEAEAGGSLDARSLRPAW ATGK
13842	27743	A	14010	123	3	KEPSRPGRWLTSTIIPACWEAEAGGPPEA RSSTREFRTAK
13843	27744	A	14011	403	168	GTGLRASRCISQPVMSGLLSPSEFPFPE IESHLHVSQRETAARLDRERERARERE RERERGNASSGKPPGSASCVP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13844	27745	A	14012	207	422	ETRRGSLAGDLSLNFILSVMSGSHSKYLRLKVGRAQWLMPPVVPALWEAEVGLHLELRRLGHTWAAW
13845	27746	A	14013	200	405	WLCVLGWSLLALSPLRECYGPTSAHCNLLHLLRSSDPASASQALQEAQYQHLLMM PQAASTQVGRKK
13846	27747	A	14014	319	176	KPSTITFLFLHLFISSRESRPVTQTEVKWLNHSSPQPPTPRFSLPSS
13847	27748	A	14015	63	401	EQENKNTLNSPGWDGVHIVLRFNLTRMPLGHLSEFSEGVSGSGSGRRQAGAGGRSATAAARPCQCLGLKGLPPAVPSCGLEG KAPERAGYSASHPPHGCETGNGWVLYVN
13848	27749	A	14016	416	63	VSKVYPKINHRTQRTVRHETFKIAMPKYYSNLCSILRFNDRALAFMRHYTKQCSRTS ITEYIAMFFVFCLFVLKIGAHCHPGWNE VVLVCSQVTAASTSRAQAILPPQPPKIL GMQQA
13849	27750	A	14017	196	425	SLMFRPPLFSFCCFCIRYPIFVFFSLL CFAFSWCSLLFFFFHYLKLFLLLFLFF LPVLLCLDSFLVHDFLLSS
13850	27751	A	14018	3	233	SSRMGRGKTIAFDMRWSCEVDRARHRDREREREREREREREKGAEPQEFPPVISPWDRPCLAGILHLKCGCGHRL
13851	27752	A	14019	163	1	AERWHDQICVEREIWGWVQWLMPIVPLWEAKAKNLEPKNLKLQRNRRPGNSR
13852	27753	A	14020	203	83	LKKKKKNKSQAQWLTSSVVLASQEAEGGSLEPRNSRPAAWAT
13853	27754	A	14021	179	3	VTWQRELRLQMEIIRLLICRAWLTPVIPVPWEAKAGGSPEPRSSRPAAWETRNRPGNS
13854	27755	A	14022	358	431	WHKKKNQNLGTGAHACNPFSTLGG
13855	27756	A	14023	98	3	GRPAGWLTTPVAPTLLWEAEMGGSLEPRSLGHE
13856	27757	A	14024	254	385	RENWAEPPSSHLLNIFLQLGTVARACNPSTLGGRGGWITRSGD
13857	27758	A	14025	140	1	KGVLGPRGLCVFCFCFFFLCVCVCVCVCVCVWRSLTSLPRLOCI
13858	27759	A	14026	579	852	QREWVGWAGKEGEGWVSHVPASQAQLPAN GQRGQPHPSPLGGTGSTWAQEGAYCCLS SCSHCCCCSSCCCCPPGFCLFPLSGAICHLYHL
13859	27760	A	14027	30	663	LRIRALRELPAISHIPGSLTICCVPRPPLPCSSSTKPDAGYKPLAQKLGSGRTGPC LGHAPCYSPLWELRGHGCSFYGPSPSGS VSLWQEAAMRLPKNTPBEKDRRTAALQEG LRRAVSVPLTLAETVASLWPALQELARC GNLA CRSDLQVAAKALEMGVFGAYFNVL INLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCLETRQE
13860	27761	A	14028	1	267	AVGVHHAFLPHCFASLLESPVSPRLA MDPNCSCAAGVSCTCAGSCKCKECKCTSCSKSCSCCPVGCCKAQCVCCKGASEK CSCCD
13861	27762	A	14029	46	1746	PAAGAATMEFRQEEFRKLALGKLRHRLLEKRGEGAEITLSEADGRPVTTQTRDP PVVDCTCFGLPRRYIIAIMSGLGFCISF GIRCNLGVAIVSMVNNSTHRRGHVVVQKAQFSWDPETVGLIHGSFFWGYIVTQIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGFICQKFAANRVFGFAIVATSTLNMLI PSAARVHYGCVIFVRILQGLVEGVITYPA CHGIWSKWAPPLERSRLATTAFCGSYAG AVVAMPLAGVLVQYSGWSSVFYVYGSFG IFWYLFWLLVSYESPALHPSISEEERKY IEDAIGESAKLMNPLTKFSTPWRFFTS MPVYAIIVANFCRSWTFYLLISQPAYF EEVFGFEISKVGLVSALPHLVMITIVPI GGQIADFLRSRRIMSTTNVRKLMNCGGF GMEATLLLVVGYSHSKGVAISFLVLAVG FSGFAISGFNVNHLDIAPRYASILMGIS NGVGTLSGMVCPPIVGMATKHKTREEWQ YVFLIASLVHYGGVIFYGVFASGEKQPW AEPEEMSEEEKCGFVGHDQLAGSDDSEME DEAEPPGAPPAPPPSYGATHSTFQPPRP PPPVRDY
13862	27763	A	14030	240	63	VFTAQSNNGVELNRFNEGPLSAVLKGRV AWAQWLTPIPTLWEVKAGGLLEARSLS PA
13863	27764	A	14031	289	414	HAEMGRVQWLTPAIPALCKAEAGGPPEP RSLRPAWATY
13864	27765	A	14032	386	1765	LGDARAPEKMSAIIQAAWPSGTECIAKYN FHGTAEQDLFPCKGDVLTIVAVTKDPNW YKAKNKVGREGIIPANYVQKREGVKAGT KLSLMPWFHGKITREQAERLLYPPEGL FLVRESTNYPGDYTLVCSDGKVEHYRI MYHASKLSIDEDEVYFENLMQLVEHYTSD ADGLCTRLIKPKVMEGTVAQAQDEFYRSG WALNMKELKLLQTIGKGFVDVMLGDYR GNKVAVKCIKNATAQAFLAEASVMTQL RHSNLVQLLGVIVEEKGGLYIVTEYMAK GSLVDYLRSGRSVLGGDCLLKFSLDVC EAMEYLEGNNFVHRDLARNVLVSEDNV AKVSDFGLTKEASSTQDTGKLPVKWTAP EALREKKFSTKSDVWSFGILLWEIYSFG RVYPYPRIPKDVVPRVEKGYKMDAPDGC PPAVYEVKNCWHLDAAMRPSFLQLREQ LEHIKTHELHL
13865	27766	A	14033	619	414	EQARCLEQHACTSPRQPRQLQCSELKG HSLGMEHQGHVPCPLHPCSPCPPVKASPA CWSSNPAPLCPH
13866	27767	A	14034	2	614	LESRPDGRPSSTHPASPSAFSAPGKPHP PEAKMSSKRAKAKTTKKRPQRATSNVFA MFDQSQIQEFKEAFNMIDQNRDGFIDKE DLHDMLASLGKNPTDEYLEGMMSEAPGP INFTMFLTMFGEKLNQTDPELVIRNAFA CFDEEASGFIEDHLRELLTTMGDRFTD EEVDEMYREAPIDKKNFNHYVEFTRILK HGAKDKDD
13867	27768	A	14035	1	254	AVEFGPAGPGSLGRAAAMIIPVRCFTCG KIVGNKWEAYLGLLQAEYTEGDALDALG LKRYCCRRMLLAHVDLIEKLLNYAPLEK
13868	27769	A	14036	494	148	FRFLSDCGVFAEGHIELQVESGVPLGFS TMAEDMETKIKNYKTAPFDSRFPNQNT RNCWQNYLDFHRCQKAMTAKGGDISVCE WYQRVYQSLCPTSWTWDWEQRAEGTFP GKI
13869	27770	A	14037	130	3969	IMGDVKNFLYAWCGKRKMTPSYEIRAVG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NKNRQKFMCEVQVEGYNTGMGNSTNKK DAQSNAARDFVNYLVRLINEIKSEEVPAF GVASPPPLTDTPTTANAEGDLPTTMGG PLPPHLALKAENNSEVGASGYGVPGPTW DRGANLKDYYSRKEEQEVQATLESEEVD LNAGLHGNWTLNNAKARLNQYFQKEKIQ GEYKYTQVGPDHNRSFIAEMTIYIKQLG RRIFAREHGSNNKLAQSCALSLVRQLY HLGVEAYSGLTKKKEGETVEPYKVNLS QDLEHQLQNLIQELNLEILPPPEPSVP VALNIGKLAQFEPSQRQNVGVVPWSPP QSNWNPWTSNIDEGPLAFATPEQISMD LKNELMYQLEQDHDQLAILQERELLPVK KFESEILEAISQNSVVIIRGATGCGKTT QVPQFILDDFIQNDRAAECNIVVTQPRR ISAVSVAERVAFERGEEPGKSCGYSVRF ESVLPRPHASIMFCTVGLLRKLEAGIR GISHVIVDEIHERDINTSFLLVLRDVV QAYPEVRIVFMSATIDTSMFCEYFNCP SLKLWRTYPVQEFLEDCIQMTHFVPPP KDKKKKDDDDGGEDDANCNLCGDEY GPETRLSMSQLNEKETPFELIEALLKYI ETLNVPGAVLVFLPGWNLIYTMQKHLE NPHFGSHRYQILPLHSQIPREEQRKVFD PVPVGVTKVILSTNIAETSITINDVVYV IDSCQKVKLFTAHNNMNYSTVWASKT NLEQRKGRAGRSTAGFCFHLCSRARFER LETHMTPEMFRTPLHEIALSIKLLRLGG IGQFLAKAIEPPPLDAVIEAHTLRELD ALDANDELTPGLRILAKLPIEPFRGKMM IMGCIFFYVGDAICTIAAATCFPEPFVNE GKQLGYIHRNFAGNRFSDHVALLSVFQA WDDARMGGEAEIRFCEHKRLNMATLRM TWEAKVQLKEILINSGFPEDCLLTQVFT NTGPDNNLDVVISLLAFGVYPNVYHKE KRKILTTEGRNALIHKSSVNCPSQDM NYPSPPFFVGEKIRTRAISAKGMTLVPP LQLLLFASKKVQSDGQIVLVDDWIKLQI SHEAAACITGLRAAMEALVVEVTQPAI ISQLDPVNERMLNMIROISEPSAAGINL MIGSTRYGDGPRPPKMARYDNGSGYRRG GSSYSGGGYGGYSSGGYSGGGYGGSAT PSGRICAGVGGYRGVSRGGFRGNSGGD YRGPSGGYRGSGGFQRGGGRGAYGTGYL DIEEEVAAIKLGYVSSVCRQ
13870	27771	A	14038	431	542	EGITPGWARWLTPTVPIGLWEEERAGGSPG REIDIGLAN
13871	27772	A	14040	238	362	RRCTFLSFRMLAPRVYSVVGKRAFSPSV CVRAHGKCDYSYS
13872	27773	A	14041	6290	3514	FRAAGSSSTNSGRICPLPSGALLYQSEG LLARPHGKGSFQVGRQQHQAIVRGSAAH SSAGYVCVSAPFPVFLRFCVGGGPGISR VYALFYGECNPTREWAVSSELSPSFQEQ NKMNKVEQKSQESVSFKDVTVGFTQEEW QHLDPSQRALYRDVMLENYSNLVSVGYC VHKPEVIFRLQQGEEPWKQEEFFPSQSF PEVWTADHLKERSQENQSKHLWEVVFIN NEMLTKEQGDVIGIPFNVDVSSFP SRKM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FCQCDSCGMSFNTVSELVISKINYLGKK SDEFNACGKLLLNLIKHDETHTREKNEVL KNRNTLSHRENTLQHEKIQTLHDNFEYS ICQETLLEKAVFNTRKRENAEENNCDDYN EFGRTFCSSSLLFHQISPSRDNHYEFS DCEKFLCVKSTLSKPHGVSMKHYDCGES GNNFRRLCLSHLQKGDKEKHFECNEC GKAFWEKSHLTRHQRVHTGQKPFQCNAC EKAFWDKSNLTKHQRSHTEGKPFECNEC GKAFSHKSALTTLHQRTHTEGKPYQCNA GETFYQKSDLTKHQRTHTEGKPYECYEC GKSFCMNSHLTVHQRTHTEGKPFECLEC GKSFCQKSHLTQHQRTHIGDKPYECNA GKTFYHKSVLTRHQIHTGLKPYECYEC GKTFCLKSDLTIHQRTHTEGKPFACPEC GKFFSHKSTLSQHYRTHTEGKPYECHEC GKIFYNKSYLETKHNRTHTEGKPYECNEC GKTFQCQSQTQHQRTHIGDKPYECNEC GKAFCHKSAALIVHQRTHTEGKPYECNEC GKSFCVKSLIFHERKHTGKPYECNEC GKFFRHKSSSLTVHHRHTGKESQCQNEC GKIFYRKSELAQHQRSHTEGKPYECNTC RKTFQSQKSNLIVHQRTHIGENLMNEMDI RNFQPVQVSLHNASEYSHCGESPDILNV Q
13873	27774	A	14043	187	422	LTIPKLHSAQEPAGPVSPPPPPSPTFQI GGRSRAEPRNQYCPQVAPVPALRGCLPL SPGEPPHDTSSPRHLTCGGIVF
13874	27775	A	14044	340	442	NKFLSWVRLIMPVIPTFWEAKVGGWLEA RSLRMQ
13875	27776	A	14045	3	1240	LVEGAAGQGVSDGARLRKCGTRSFPGSE EVLSSMARGSAFPAALWLSILCLLA LRAEAGPPQEESELYLWIDAHQARVLIGF EEDILIVSEGKMAFFTHDFRKAQQRMPA ISVNIHSMNFTWQAAGQAEYFYFSLR SLDKGIMADPTVNVPLLTGTVPHKASVVQ VGFPCLGKQDGVAAFEVDVIMNSEGNT ILQTPQNAIFFKTCQAECPPGCGRNGGF CNERRICECPDGFHGPCEKALCTPRCM NGGLCVTPGFCICPPGFGVNCDEKANS TTCFNGGTCFYPGKICPPGLEGEQCEI SKCPQPCRNGGKICGSKCKCSKGYQGD LCSKPVCEPGCAHGTCHPEPNKCQCQEG WHGRHCNKRYEASLIHALRPAGAQLRQH TPSLKKAERDDPPESNYIW
13876	27777	A	14046	18	274	YSQEVLCENNRSGVVSNIKRGWAWWQLT TTIPALWEAEVGGLEPRSLRLASPQPP QHEDYSMSYCAQPRFSLCIRGFIFYSLW F
13877	27778	A	14047	177	441	GGSHYAWNITFIETKLIAQFFCFFEMQ SCSVARLECRGAISAHCNLHLPSSNSP VMAQILKNQRKSNFDEDATLLGLSYTLL GEI
13878	27779	A	14048	136	319	DVFLLLFHSNYLFFETGSHSVSQAGVK WCDLSSLQPPPLGSSDPPTSASRVPALF FFLEF
13879	27780	A	14049	388	128	ELKLFPSYKGQSPQLSLRRYFADLTAIVS NRFTLCPSARHLAVYLLDLFMDRYDISI

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						QQLHLVALSCLLLASKYESDLHDWKF LFI
13880	27781	A	14050	262	3	VIYNYISVRPFPNIYHTFYTTL SFLYLS THTHTHTHTHTHTRQRETHVCVCIYTYM YMCMYAKWYKFTFLISGKARIHTHLHP CI
13881	27782	A	14051	149	423	YPHLC AFLLLPSISSFRAGVFFFSYLSL TAYPLTWKPPPEPATPQPTPNPPPGHPA TRGPKSALLDHSYACASAPPLGTEGTAP SPSFALI
13882	27783	A	14052	2	1440	FVAVTAMAAPCLLRQGRAGALKTMLQEA QVFRGLASTVLSAESGKSEKGPQNSK KQSPPKNVVEPKERGLLATQTAAELSK NLSSPSSYP PAVNKGKRVASPSPGSVL FTDEGVPKFLSRKTLVEFPQKVLSPFRK QGSDSEARQVGRKVTSPSSSSSSSSSDS ESDDDEADVSEVTPRVVSKGRGGLRKPEA SHSFENRAFRVTVSAKEKTL LQKPHVDI TDPEKHPQPKKKGSPAKPSEGRENARPK TTPMRSQVDEEFLKQSLKEKQLQKTFRL NEIDKESQKPFVKGPLPVHTKSGLSAP PKGSPAPAVLAEEARAEQQLQASPPGAA EGHLEKPVPEPQRKAAPPLPRKETSGTQ GIEGHLKGGQAIVEDQIPPSNLETVPVE NNHGFHEKTAALKLEAEGEAMEDAAAPG NDRGGTQEPAPVPAEPFDNTTYKNLQHH DYSTYTFLDLNLLELSKFRMPQPPSSGRES PRH
13883	27784	A	14053	177	1253	EKKRTL PVRSVT GELQGKSLSDLAAGTM DSEKKRFT EEATKYFRERVSPVHLQILL TNNEAWKR FVTAAELPRDEADALYEALK KLRTYAAIEDEYVQQKDEQFREWFLKEF PQVKRKIQESIEKLRLANGIEEVHRGC TISNVSSSTGAASGIMSLAGLVLPFT AGTSLALTAAGVGLGAASAVTGITTSIV EHSYTSSAEAEASRLTATSIDRLKVFKE VMRDITPNLLSLLNNYEATQTIGSEIR AIRQARARARLPVTTWRISAGSGGQAE R TIAGTTRAVSRGARILSATTSGIFLALD VVNLVYESKHLHEGAKSASAEELRRQAQ ELEENLMELTQIYQRLNPFCHTH
13884	27785	A	14054	1585	2099	ICVKTFFPPLALQVRMAAAEHHHSSGLPY WPYLTAETLKNRMGHQPPPTQQHSITD NSLSLKT PSERLLYPLPPSAPPSADDNL KTPPECLLTPLPPSALPSADDNLKTPAE CLLYPLPPSADDNLKTPPECLFTPLPPS APPSVDNLKTPPECVCSLPFHPQRMII SRN
13885	27786	A	14055	2	2865	ALPDGGASVASDRAEGRPAKPSKTAARE KTEGAVAAVGGGPSSFRCCYGCCHEARL GRTSLPRGVIMLTEASLSIWGWSL GIV LFLITFGPFVIFYLTFYILCFVGGGLVV TLLFGKTNSEKYLEQCEHSFLPPTSPGV PKCLEEMKREARTIKIDRRLTGANI IDE PLQQVIQFSLRDYVQYWYYT L SDDDESFL LEIROTLQNALIQFATRSKEIDWQPYFT TRIVDDFGTHLRVFRKAQQKITEKDDQV KGTAEDLVDTFFFEVEMEKEVC RDLVC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TSPKDEEGFLRDLCEVLLYLLLPFGDFQ NKIMRYFVREILARGILLPLINQLSDPD YINQYVIWMIRDSNENYAFMNI IKLS NIGELEAVRDKAAEELQYLRSLDTAGDD INTIKNQINSLLFVKVCDSRIQRLQSG KEINTVKLAANFGKLCITVPLDSILVDNV ALQFFMDYMQQTGGQAHFFWMTVEGYR VTAQQQLEVLRSQRDQKHQTNQTKGLL RAAAVGIIYEQLSEKASPRVTVDYDLVA KLADTLNHEDPTPEIFDDIQRKVYELML RDERFYPSFRQNALYVRMLAELDMKDP SFRGSDDGSGESFNGSPTGSINLSLDDL SNVSSDDSVQLHAYISDTVYADYDPYAV AGVCNDHGKTYALYAITVHRRNLNBEEM WKTYRRYSDFHDFHMRITTEQFESLSIL KLPEKKTFFNMMDRDFLEKRRKDLNAYLQ LLLAPEMMKASPALAHYVYDFLENKAYS KGKGDFAKMDTFVNPLRNSMRNVNAV KSLPDSLAEGMTKMSDNMGKMSERLQD IKQSFFKVPPLIPKTDSDPEHRRVSAQL DDNVDDNIPLRVMLLLMDEVFDLKERNQ WLRNRNIKNLQQLIRATYGDITNRKIVD HVDWMTSPEQVADSVKFRDAFWPNGIL AEAVPCRDKSIRMRTRVAGKTKLLAIMP GE
13886	27787	A	14057	311	150	FLCFKYRRGFATLHSGKLKLGSSDPPSS TSQIPGITGTSHCVQPTHLFFLALS
13887	27788	A	14058	53	211	RQHITCLDIFFIHMNYKYKYNITYLSIY LSIYLSIYLIYLSISHSYITERA
13888	27789	A	14059	1	1642	RDGRKMATATIALQVNGQQGGGSEPA AAVVAAGDKWKPPQGTDSIKMENGQSTA AKLGLPPLTPEQQEALQKAKKYAMEQSI KSVLVKQTIAHQQQQLTNLQMAAQRORA LAIMCRVYVGSIIYELGEDTIRQAFAPF GPIKSIDMSWDSVTMKHKGFAFVEYEV EAAQLALEQMNSVMLGGRNIKVGRPSNI GQAQPIIDQLAEERAFNRIYVASVHOD LSDDDIKSVEFAFGKIKSCTLRADPTTG KHKGYGFIYEKAQSSQDAVSSMNLFDL GGQYLRVGKAVTPPMPLLTPTATPGGLPP AAAVAAAAATAKITAQEAVAGAAVLGTL GTPGLVSPALTLAQPLGTLPAQVMAAQA PGVITGVTARPPIPTVTPSVGVVNPIL ASPPTLGLLEPKKEKEEEELFPESERPE MLSEQEHMSISGSSARHMVMQKLLRKQE STVMVLRNMVDPKIDDDLEGEVTEECG KFGAVNRVIIYQEKQGEEDAEIIVKIF VEFSIASETHKAIQALNGRWFAGRKVVA EVYDQERFDNSDLA
13889	27790	A	14060	1238	1474	VLALQEGRPWRREPASIDACRLNFQRLR RGKFSNVLFPGLAQEALYSGGYHLKFAD ELMGCNLKKSTADASGSRGHQL
13890	27791	A	14061	266	400	GQWARPVIPALWEAKAGGSLEPSMLRPA GQHIKTPSVLITSKKT
13891	27792	A	14062	2178	1881	VLQAPSILLAPRTDGGDMGRAMVARLG LWLLLLALLLPTQIYSETTTGTSSNSS QSTNTGLAPNPTNATTKAAGGALQSTA SLFVVSLSLLHLYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13892	27793	A	14063	261	1	NSVLTLLALLFSLHVLPPPPSGVTDTAG ALSTGGPPSPSTSVTGRGPAHSHASQLPP APGEFAPLNESCRGWAGEAFLEFRPD AWVDP
13893	27794	A	14064	2384	1115	QHFSRRGLCVVEQRSSVTSSWTS GAWSP PCPPSNASCNTLHTRD WASPD PGGQGS LGESPGP APPQGLHTLDTLHSLAQIGGK SPVAGVGNNGSLWPRES PGTANGHSPEH TPPGPGPP GPCPTKRRLLPAGEADPVSS EEEGPAPRRRRGSLGHPTA ANSSDAKAT PFWSHLLPG PKPEVLDPTDCGPMGRRLK GARRLKLSPRLSLRKG PGLLSPPRASPV PTPAVSR TLLGNFEESLLRGRFAPSG HI EGFTAIEIGASGSYCPQ HVTLPTVTFFD VSEQNAP APFLGIVDLNPLGRKGYSP VK VGTIVQVTLFNPNTV VKMFLVTFDFSDM PAAHMT FLRHRLFLVPVGEEGNAN PTHR LLCYLLHLFRSSRS RGRLSLHGDIRLLF SRRS LELDTGLPYELQAVTEAP HNPRYS PLP
13894	27795	A	14065	232	416	GWAVQLGIGTEGKEGTSSSER QREGGRD GNRKGTGRRREG RRSTKTDAPSPYPAHRP RSKLI
13895	27796	A	14067	238	45	IQTGSHSFCIPSIWEAKAG LLEPRSL SPACPTQKDP ISHLGSEL PQSFRLLIRL VPLFLSAC
13896	27797	A	14068	3	1705	SCESKATPWRAVSASQELQ HPQGGQRSP LPGDLTPAR PNPAYPLTVECQRSCSRPV PAPLPPTHPPGSSCFYSS FSFITKATA PGAORRAVT QAERGRMGLGTGTWILVL VLPFIQAFPKPGGSQDKSL HNRLESAERP LNEQIAEA EEDKIKKTYPPENKPGQSN Y SFVDNLNLLKAITEKE KIEKERQSIRSS PLDNKLN VEDVDSTKNRKLIDDYD STKS GLDHKFQDDPDGL HQLDGTPLTAEDIVH KIAARIYEENDRAVFDKIV SKLLNLGLI TESQAHTL EDEVAVLQKLISKEANNYE EDPNKPTSWTENQAGKIE KVTPMAAIQ DGLAKGEN DETVSNTLTLTNGLERRT KT YSEDNFEELQYFPN FYALLKSIDSEKEA KEKETLITIMKTLIDFV KMMVKYGTISP EEGVSY LENLDEMIALQTKNKLE KNATD NISKLFPA PSEKSHEETDSTKEEA AKME KEYGSLKDS TKDDNSNPGGKTDE PKGKT EAYLEAIRK NIEWLKKHDKKGNK EDYDL SKMRDFIN KQADAYVEKGILDKEA EAI KRIYSSL
13897	27798	A	14069	1	140	NTSVAIQTI EYSAF KRKETLTHVPLWM NLKDTMLREISQS QKDTV
13898	27799	A	14071	212	104	HTNHQCQT VLPAGQALATPQGLAP SPVF PQSCLRMV
13899	27800	A	14072	358	112	FPLTVMLNVFLWQNLK HFCWFIEQQLM FFFFFFLRTGSHYVQAG LELLGSTNLP ASVSRV AGTTGIHNCTQFNPL HTLHL
13900	27801	A	14073	3	151	YMGFHHVGYAGLELLT SSDLPPWPPKCW DYRHEPSCLAMFFYF ALIAPE
13901	27802	A	14074	8	1493	VTIHHLFV GQAVRADTLKKKSP SCLLCI VFIPVPRID LTNIDQVAVIFKHH FPVGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						GDAVLK TWAPAQCLCSRMGP AWLWL LGT GILASVHCQPLLAHGDKSLQGPQPPRHQ LSEPAPAYHRITPTITNFALRLYKELAA DAPGNIFFSPVSI STLALLSLGAQANT SALILEGLGFNL TETPEADIHQGFRLSL HTLALPSPKLELKVGNSLFLDKRLKPRQ HYLD SIKELYGAFAFSANFTDSVTTGRQ INDYLRRQTYGQVVDCLPEFSQDTFMVL ANYIFFKAKWKHPFSRYQTQKQESFFVD ERTSLQVPMMHQKEMHRFLYDQDLACTV LQIEYRGNALALLVLPDPGKMKQVEAAL QPQTLRKWGQLLLPSLLDLHLPRFSISG TYNLEDILPQIGLTNINLEADFGVGTG QLNKTI SKVSHKAMVDMSEKGT EAGAAS GLLSQPPSLNTMSDPHAHFNRPFLLLLW EVTTQSLFLGKVVPVAG

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-13901 , a mature protein coding portion of SEQ ID NO: 1-13901 , an active domain of SEQ ID NO: 1-13901 , and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NOS: 1-13901.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-13901, a mature protein coding portion of SEQ ID NO: 1-13901, an active domain of SEQ ID NO: 1-13901, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-13901, under conditions sufficient to express the polypeptide in said cell; and
- b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS: 13902-27802, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NOS: 1-13901.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

5 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

10 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.